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Title:
Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1729
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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e cinium OCAFADAK	Y13831 Erwinia amy	U94513 Erwinia amy	U16119 Pseudomonas	AF037983 Pseudomon	AF232004 Pseudomon	Af232006 Pseudomon	AF005221 Pseudomon	Description		

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MEDLINE
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AUTHORS
TITLE
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DEFINITION
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57
                                           Submitted Ithaca, NY
                                                                                    The Pseudomonas syringae pv. tomato HrpW protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate J. Bacteriol 180 (19), 5211-5217 (1998)
                                                         Direct Submission
                                                                Charkowski, A.O.,
                                                                                                                      1 (bases 1 to 1729)
Charkowski, A.O., Alfano, J.R.,
                                                                                                                                                                         AF005221
AF005221.1
                                                                                                                  Collmer,A.
                                                                                                                                              Pseudomonas syringae
Bacteria; Proteobacteria;
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                                          ed (23-MAY-1997) Plant
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/strain="DC3000"
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        /db_xref="taxon:317"
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                                                 Pathology, Cornell University,
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                                                                                                                       Yuan,J.,
                                                                                                                                              Pseudomonadaceae;
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AL136332 Homo sapi
AC091196 Homo sapi
AL021999 Mycobacte
AL021897 Mycobacte
X17207 Chlamydomon
AL021841 Mycobacte
AB025226 Gallus ga
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E32986 Gene encodi
AC019585 Drosophil
AC009388 Drosophil
AE003763 Drosophil
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AL022004 Mycobacte
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Ac009249 Drosophil
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AC090435 Chlamydom
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charkowski A.O., Alfano J.R., Preston G., "The Pseudomonas syringae pv. tomato HrpW harpins and pectate lyases and can elicit and bind to pectate";
J. Bacteriol. 180(19):5211-5217(1998).
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1-20052
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PUBMED; 10781092.
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Bacteria; P
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                                                                                                                                                                   SPTREMBL;
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                                                                                                                                                                                                                                 SPTREMBL;
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                                                                                                                                                                                      Q9JP36;
Q9JP37;
                                                                                                                                                                                                                                                Q9JP33;
Q9JP34;
                                                                                                                                                                                                                                                                                        Q9JP31;
Q9JP32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (07-FEB-2000)
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Proteobacteria;
                                                                                                                                                                                                                               Q9JP35;
                                                                                                                                                                                                                                                                                                                                   Q9JP30;
                                                                                                                                                                                                                                                                                                                                                        Q9JP29;
                                                                                                                                                                                                                                                                                                                                                                           Q9JP28;
                                                                                                                                                                                                                                                                                                                                                                                            Q9лР27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collmer A.;
/note="conserved effector locus
cluster pathovar: tomato"
/organism="Pseudomonas syringae
                                                             1. .20052
/db_xref="taxon:323"
                                                                                                                         Location/Qualifiers
                                                                                                                                                                                    066101
087264
09JP27
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Last updated,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases 1854 Maryland Parkway, Las Vegas, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tomato; gamma
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DWLLSNRGFITGASVRASPYLHFIVERLDERNMPLELALLPHIESSYNPMANSPAAAGE
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GTVGRAIEANRRRGLPVDYWLINLPRETQDYVPRLLALSWVVNUPNAXYGVKLTPVANTP
YFDVYELNHAVDLTQLAATAGYDEGGLLRLNSAFLRKKTEDGPGRLLIPKTQNRVLTTS
IARITGESPVTASIFLYTESAIVKRAAERLPAPAPVAERPVRVAERPPLFKFVQSAQLA
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                                                                                                                                                                                                                                                                                          complement (8226.
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VGKRALKSVGKLFQKSKAPQQKAATPPTAKNVKTPPPASNVATPRNKARESGFSNSSPQ
NTHAAPKWILRNHPNQASSSGAQTHBIHPEAAPRKNLRVRFDLPQDRLERSPSYLDSDN
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                                                                                                                  complement(8960. .10831)
                                                                                                                                       SLDEPAFCDVTRGFISQAREARAFLQA"
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/product="AvrE"
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                                                                                      /db_xref="SPTREMBL:Q9JP36"
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                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q9JP37"
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                                                    transl_table=11/
                                                                                                                                                                                                        'product="unknown"
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cctctgagtgcggtgcggagcaataccagtcttcctgctggcgtgtgcacactgagtcgc
                                                                                                    CTGAGTGCGCAGATTTCGTTGATAAGGGTGTGGTACTGGTCATTGTTGGTCATTTCAAGG
                                                    ctgagtgcgcagatttcgttgataagggtgtggtactggtcattgttggtcatttccaagg
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Conservative

0;

Indels Length

Gaps

0;

11329 120 11269 60 99.88;

Score 1725.8; Pred. No. 0; Mismatches

DВ 2; 16;

20052; 0;

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DQVGTKMMDRATGDLHYLSASPDRLHDAMAASVKRHSPSLARQVLDTGVAVQTYSARNA
VRTVLAPALASRPAVQGAVDLGVSMAGGLAANAGFGNRLLSVGSRDHQRGGALVLGLKS
VRTVLAPALASRPAVGGAVDLGVSMAGGLAANAGFGNRLLSVGSRDHQRGGALVLGLKS
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EPLPPEVMAEKLSPERYQLKQFQGSDLQQKLEKFAQPGQIPDKAEVGQLIKGFAQSVAD
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QLEHFQLMHDASPATVGQHAKADKATLAVDAKTTLVGLHADEVKSPEAKRLSVAAHTQLD
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NVVSDLVTARNTVGGWKGAGPIVAAAVPQFLSSMTHLGYVRLSTSDKLRDTIPETSSDA
NMLKASIIGNVAGIAHETVNSVVKPMFQAALQKTGLNERLNMVPMKAVDINTVIPDFFE
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LFGSSTQKDVMEGTPDSTVQNPQDASKPNDSQSNTAKLISALIMSLLQMINSNKKQDT
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SGGGGTPTATGGGSGGTPTATGGGEGGGTPDGITGGGGDTPSATGGGGGTPQAG
KINVVKDTIKKGAGEVFDGHGATTANHAGNVGDLTTVKSEGGAAVUNLNIKNSSAGADLKVVNLGEN
EVDGJHVKAKHAQEVTIDAVHAGNVGEDLTTVKGEGGAAVUNLNIKNSSAGADLKVVD
LNANTHLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLA
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RDEGRAVLIYGDMGALPARGRESALLALMDINFHMFAGAHSPAFSFNAQTGRVLLMGSV
ALERASAEGVLLLMKSFSDLAKEWREHGFMGQATTAGSSTDQPVAPAAKRESLSAPGRF
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QMLNDYHQINGQTLSARALASGFGGAVSASSQTLLQLKSNYYDPQGRKIPYFTDDRAES
DLKKDLLKGNDLREPSYRTTFYSKALSGIQSSALTSALPPYTAQABGASGTLSAGAILR
                                                                                                                                                                                                           KEPKAQLSEENDWLEAYKAIKSASYSGAALNAGKRMAGLPLDMATDAMGAVRSLVSASS
LTQNGLALAGGFAGVGKLQEMATKNITDPATKAAVSQLTNLAGSAAVFAGWTTAALTTD
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                                                                                                                                                                PAVKKAESFIQDTVKSTASSTTGYVADQTVKLAKTVKDMGGEAITHTGASLRNTVNNLF
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db_xref="SPTREMBL:Q9JP33"
                                              /codon_start=]
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similar to harpins and pectate lyases and can hypersensitive response and bind to pectate J. Bacteriol. 180 (19), 5211-5217 (1998) 98422476
                                                                                                                        2 (bases 22134 to 25847; 29687 to 32670)
Deng,W.L., Preston.G., Collmer.A., Chang.C.J. and Huang,H.C.
Characterization of the hrpC and hrpK operons of Pseudomonas
syringae pathovars syringae, tomato, and glycinea and analysis
the ability of hrpF, hrpG, hrcC, hrpT, and hrpV mutants to eli
the hypersensitive response and disease in plants
J. Bacteriol. 180 (17), 4523-4531 (1998)
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                                                          Collmer, A.
The Pseudomonas
                                                                                   Charkowski, A.O.,
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Preston,G., Huang,H.C., He,S.Y. and Collmer,A.
The HrpZ proteins of Pseudomonas syringae pvs.
and tomato are encoded by an operon containing
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Pseudomonas syringae pv. tomato
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Sequence update by submitter
On Mar 14, 2001 this sequence version replaced gi:3228544 gi:790906
gi:3228541 gi:8037790 gi:11276506.
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Direct Submission
Submitted (05-MAR-2001) Plant Pathology, Cornell University, 334
Plant Sciences Bldg., Ithaca, NY 14850, USA
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Alfano,J.R., Charkowski,A.O., Deng,W.L., Badel,J.L.,
Petnicki-Ocwieja,T., van Dijk,K. and Collmer,A.
The Pseudomonas syringae Hrp pathogenicity island has a tripartite mosaic structure composed of a cluster of type III secretion genes bounded by exchangeable effector and conserved effector loci that contribute to parasitic fitness and pathogenicity in plants proc. Natl. Acad. Sci. U.S.A. 97 (9), 4856-4861 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mrvadftfeelpdsliarhplaerrssrlltldgptgalahrqft
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pgssilidgggeaemvarhdalfelrfaeevlplldrvghmplppyidrpdegadrer
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/gene="queA"
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/db_xref="taxon:323"
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                                                                     TTTTTTTGCTGGCGTGTACGCACTGAGTCGGAGGGCAAGGGGTTTTGGTTCCTTGGGGCG
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Science Bldg. Rm 334, Ithaca, NY 14853, U
Location/Qualifiers
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Pseudomonas syringae pv. syringae
Bacteria; Proteobacteria; gamma subdivision;
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/protein_id="AaC62530.1"
/protein_id="AaC62530.1"
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SALLEDTARQKDVSFGQDDNTYQNFTDSSAATDPQSNVVKLLSALVTSLLQMLMNLNK
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PTTEGDGGGTSPTAEGDGGGSYVSTGADGSGAPSTEDGTGGGGGSDGYTPQVTPQLAN
PGRNAGGNGTVSDTTGSLEQSGEVNVKDTIKVGAGQVFDGHGATFTADKSMGTGDQDE
HQKPLFELAEGAVLKNVLGEBEADGIHVNAKNSEQVTIDNVHAQNVGEDMITVKGEG
GAKVTNLNITNSSANGADDKVIQLNADTHLKVDGFKATDFGTLVRTNGGKQFDDMSVE
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/function="pectate binding"
/note="HrpW; harpin"
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U16119.1
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Lorang, J.M. and Keen, N.T.
Characterization of avrE from
hrp-linked avirulence locus co
                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                         Keen, N.T
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Location/Qualifiers
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                                                                                                                /translation="MPLTSSKLNPKHPHPYRTDSDTATCSGKPWSWRRSNCPLSEVTQ HEHRHHTPAATDHAARFFGAKRQESSTKHVRRAEHSASDRPECTVVRQRHTERRQLR HARQHRPESAGRQQAQRQPVQHR"
198 c 185 g 146 t
                                                                                                                                                           /evidence=not_experimental
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/db_xref="GI:563241"
                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                              /organism="Pseudomonas
/db_xref="taxon:323"
                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                          /note="avrE locus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:563240
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syringae pv. tomato
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                                                    Score 692.2;
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Riverside, CA 92521, USA
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3 (bases 1 to 2708)
Kim,J.F. and Beer,S.V.
Direct Submission
Submitted (18-MAR-1997)
                                                   Kim,J.F. and Beer,S.V.
HrpW of Erwinia amylovora, a new harpin that contains homologous to pectate lyases of a distinct class J. Bacteriol. 180 (19), 5203-5210 (1998)
                                                                                                                  1 (bases 912 to 2255)

Kin, Jr., Zumoff,C.H. and Beer

HrpW, a new harpin of Erwinia

pectate lyases
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Erwinia amylovora disc
hrpW operon, complete
                                          98422475
                                                                                             Phytopathology 87, S52 (bases 1 to 2708)
                                                                                                                                                            Erwinia.
                                                                                                                                                                              Erwinia
                                                                                                                                                                                           Erwinia amylovora.
                                                                                                                                                                                                   type III protein secretion; pectate lyase.
                                                                                                                                                                                                                        U94513.1 GI:3414585
                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                              amylovora
                                                                                                                                                                                                                                       8 bp una a disease-specific capital sequence.
                                                                                                        (1997)
 Plant Pathology, Cornell University,
                                                                                                                                       Beer, S.V.
                                                                                                                                                                      gamma
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                                                                                                                             amylovora,
                                                                                                                                                                      subdivision;
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                                                                                                                                                                                                                                  /product="Hrpw"
/product="Hrpw"
/protein_id="AaC62314.1"
/protein_id="AaC62314.1"
/db_xref="Gl:3414586"
/db_xref="Gl:3414586"
/translation="MSILTLINNNTSSSPGLFQSGGDNGLGGHNANSALGQQPIDRQTI
/translation="MSILTLINNTSSSPGLFQSGGDNGLGGHNAGILLREKGTAGTTPQSDSQN
MLSEMGNNGLLAELLKSLLSPQSGNAATGAGGNDQTTGVGNAGGLNGRKGTAGTTPQSDSQN
MLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARMDGQSDQFQGTGNNSA
SGTSSSGGSPTNDLSGGKAPSGNSPSGNYSPVSTFSPFSTFTSTSPLDFPSSTTKA
AGGSTFYTDHPDPVGSAGIGAANSVAFTSAGANQTVJHDTITYKAGQVFDGKCGTFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="DspE"
/protein_id="Aac62315.1"
/protein_id="Aac62315.1"
/db_xref="q:3414587"
/translation="MELKSLGTEHKAAVHTAAHNPVGHGVALQQGSSSSSPQNAAASL
/Aacgkrrgkrerihopstaadoisaahookksfslagcigteksrspapogopgtths
KGATLRDLLARDDGETGHEAAAPDAARLTRSGGVKRRNMDDMAGRPMVKGGSGEDKVP
TQQKRHOLNNFQOMRQTMLSKWAHPASANAGDRLQHSPPHIPGSHHEIKEEPVGSTSK
ATTAHADRVEIAQEDDDSEF"
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/translation="mmmksaeippaeswvDvvnsQQHLspaQvQafQkaiDQvQQRLH
QVLSRPmPQRQGKFELDSFvDSLHADFLIGDSDRSDSNVGQTAWWITRVLADRLLELQ
                                                                                                                                                                                   ITVKPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFVRTNGGQQ
GNWDLNLSHISAEDGKFSFVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKVAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Hrp-secreted pathogenicity/avirulence
similar to Pseudomonas syringae AvrE"
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/gene="dspE"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="disease-specific complement(<1...729)
                                 /product="potential HrpW-specific
/protein_id="AAC62316.1"
/db_xref="GI:3414588"
                                                                                                                                                                                                                       GSELGDGGQSENQKPLFILEDGASLKNVTMGDDGADGIHLYGDAKIDNLHVTNVGEDA
                                                                                                                                                                                                                                                                                                                                                                                                                         cysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="hrpW"
/function="elicit the hypersensitive reaction"
/note="Hrp-secreted; C-terminal domain similar to class
/note="Hrp-secreted; C-terminal domain similar to class
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="disease-specific operon"
/note="HrpL-dependent promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="dspE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="dspE"
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/db_xref="taxon:552"
/db_xref="ATCC:49947"
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                                                                                           /transl_table=11
                                                                                                                             /note="putative;
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                                                                                                            codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATCCCACGTTGAAATCACTAACAGTTCCTTCGAGCACGCCTCTGACAAGATCCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCACGTCACCAACGTGGGTGAGGACGCGATTACCGTTAAGCCAAACAGCGCGGGCAAA 1943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cagaagcccatgttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggtgag 1258
                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGATATCTCACTGGGTGATGTTGAAAACCACTACAA 2218
                                                                                                                                                                                                                                                                                                                                                                                                                                              ggcaacatcgccatgaccgacgtcaaacacgcctacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGAAGACGGTAAGTTCTCGTTCGTTAAAAAGCGATAGCGAGGGGCTAAACGTCAATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gctaaccacggcaagttcgccctggtgaaaagcgacagtgacgatctgaagctggcaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACGCACTAACGGCGGTCAACAG----GGTAACTGGGATCTGAATCTGAGCCATATCAGC 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gttcgcaccaacggtggcaagcagtttgatgacatgagcatcgagctgaacggcatcgaa 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctcaacgccaacactcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatg 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcactaatctgaacatcaagaacagcagtgccaaaggtgcagacgacaaggttgtccag 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aacgaggtcgatggcatccacgtgaaagccaaaaacgctcaggaagtcaccattgacaac 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAAACCGCTGTTTATACTGGAAGACGGTGCCAGCCTGAAAAACGTCACCATGGGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAAAGGACAAACCTTCACCGCCGGTTCAGAATTAGGCGATGGCGGCCAGTCTGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggccacggcgcaaccttcactgccgacaaatctatgggtaacggagaccagggcgaaaat 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gccggcaagatcaatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgac 1138
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                                                                                                                                                                                                                                                                                              Erwinia
Y13831
Direct Submission
                                                                                                            DspA, an essential pathogenicity factor of Erwinia amylovora showing homology with AvrE of Pseudomonas syringae, is secre
                                                                                                                                                                                                                                     dspA gene; dspB gene;
Erwinia amylovora.
                      Gaudriault,S.
                                                                                         the Hrp secretion pathway in a DspB-dependent way
                                                                                                                                              Gaudriault, S., Malandrin, L., Paulin, J.P.
                                                                                                                                                                                   Erwinia
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                                                                                                                                                                                                                                                                             Y13831.1
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                                     (bases 1 to 9985)
                                                                                                                                                                (bases 1 to 9985)
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/gene="hrpW
a 768 c
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57.1%;
                                                                        26
                                                                                                                                                                                                                                                                                                              hrpW,
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Pred. No. 2.7e-
0; Mismatches
                                                                                                                                                                                                                                                        hrpW
                                                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                    gamma subdivision;
                                                                                                                                                                                                                                                          gene;
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                                                                                                                                                                                                                                                                                                              dspB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614
                                                                                                                                                                                                                                                        promoter
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                                                                                                                                                                                                                                                                                                              genes
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                                                                                                                                               Barny, M.A.
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Gaudriault,S., Brisset,M.N. and Barny,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-JUN-1997) S. Gaudriault, INRA, 16 rue Claude Bernard 75231, Paris, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-MAY-1998) S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                            /transl_table=11
/product="DspA protein"
/protein_id="CAA74156.1"
/protein_id="CAA74156.1"
/protein_id="CAA74156.1"
/protein_id="CAA74156.1"
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/db_xref="G1:2695858"
/db_xref="G1:2695858"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="Spfremb::054508"
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SGGTSSSGGSPENDLSGGKAPSGNSPSGNYSPVSTFSPPTSPTSPTSPLDFPSSPTKA
AGSTPVTDHPDPVGSAGIGACHSVAFTSAGANQTVLHDTITVALGQVPDGKKQTFTA
GSELGDGQGSENQFPLFILEDCASLKNVTMGDDGADGIHLYGDAKIDNHYNTWGDDA
ITVKPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDPGTFVRTNGGQQ
GNWDLNLISHISAEDGKFSFVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKVAE"
KSYSVDQRGQVAILTDTPGRHKMSIMPSLDASPESHISLSLHFADAHQGLLHGKSELE
AQSVAISHGRLVVADSEGKLFSAAIPKQGDGNELKMKAMPQHALDEHFGHDHQISGFF
HDDHGQLNALVKNNFRQQHACPLGNDHQFHPGWNLTDALVIDNQLGLHHTNPEPHEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="HrpW protein"
/protein_id="CAA74158.1"
/db_xref="GI:3150150"
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/gene="dspA"
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/transl_table=11
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/db_xref="taxon:552"
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/strain="CFBP1430"
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.3035)
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BASE COUNT
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Best Local Similarity
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                                 ctcaacgccaacactcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatg 1498
                                                                                                                                                                 gtcactaatctgaacatcaagaacagcagtgccaaaggttgcagacgacaaggttgtccag 1438
                                                                                                                                                                                                                                                                                    aacgaggtcgatggcatccacgtgaaagccaaaaacgctcaggaagtcaccattgacaac 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAAACCGCTGTTTATACTGGAAGACGGTGCCAGCCTGAAAAACGTCACCATGGGCGAC
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CTGAATGCCGATACTAACCTGAGCGTTGACAACGTGAAGGCCAAAGACTTTGGTACTTTT 1797
                                                                                                                                AAATCCCACGTTGAAATCACTAACAGTTCCTTCGAGCACGCCTCTGACAAGATCCTGCAG
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FNETMSTERPIKNAATATQHGRQGREGLKELYEMQGALIKQLDAHNVRHARPQEDLQS
KLETLDLGEHGAELLMDMKRERDELEDGSATRSVTVLGOHQGVLKNGE NSEERSEBG
KALVQSENVNRSGQDLSKSLQQAVHATPPSAESKLQSMLGHFVSAGVDMSHQKEIPL
GRQRDPNDKTALTKSRLILDTVTIGELHELADKAKLVSDHKPDADQIKQLRQQEFVTR
EKRYESUPVKHYTDMGETHNKALEANVDAVKAFINAFKKEHHGVNLTTRTVLESQGSA
ELAKKLKNTLLSLDSGBSMSFSRSYGGGVSTVFVPTLSKKVPVPVIPGAGITLDRAYN
LSESRSTSGGLMVSFGRDGGVSGNIMVARGHDVMPYMTGKKTSAGNASDMLSAKHKISP
DLRIGAAVGGTLQGTLQNSLKFKLTEDELPGFIHGLTHGTLTPAELLQKGIEHQMKQG
SKLTFSVDTSANLDLRAGINLMSDGSKPNGVTARVSAGLSASNALAAGSSRERSTTSGQ
FGSTTSASNARPTFLMGVGAGANLTAALGVAHSSTHEGKPGIFPAFTSNVSAALAL
DNRTSOSISLELKRAEPVTSNDISELTSTLGKHFKDSATTKMLAALKELDDAKPAEQL
HILQQHFSAKOVVGDERYEAVRLKKLVIRQQADSHSMELGSASHSTTYNNLSRINN
DGIVELLHKHFDAALPASSAKRLGEMANNDPALKDIRGVSGSASHSSTTSNNELKOGL
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HILQQHFSAKOVVGDERYEAVRLKKLVIRQAADSHSMELGSASHSTTVNLLSRINN
DGIVELLHKHFDAALPASSAKRLGEMANNDPALKDIRGVSGSASHSTVNELKDGL
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/gene="dspB"
8724. .9143
/gene="dspB"
/function="involved i
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SLEHLDEASFSDIVSGFIEHAAEVREYIAQLDESSAA"
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AESSSWHKLALPQSESKLKSLDMSHEHKPIATFEDGSQHQLKAGGWHAYAAPERGPLA
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/protein_id="CAA74157.1"
/db_xref="GI:2695859"
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Pred. No. 2.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF083620 4291 bp DNA BCT 12-APR-2000 Erwinia amylovora harpin HrpN (hrpN) gene, partial cds; potential ORFB-specific chaperone, virulence/avirulence effector protein homolog, probable HrpW-specific chaperone, and harpin HrpW genes, complete cds; and Hrp-secreted pathogenicity/avirulence protein DspE (dspE) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-AUG-1998) Plant Pathology, Co
Plant Science Bldg., Ithaca, NY 14853, USA
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Kim,J.F., Zumoff,C.H. and Beer,S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comparison of the hrpN-flanking regions standing with different host specificity members.
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Location/Qualifiers
Salmonella enterica, and pseudotuberculosis"
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                                                                                                                                                                                                                                                                     chaperone-like proteins;
/codon_start=1
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                 /note="ORFB; similar to ORFB of Erwinia amylovora
AvrRxv of Xanthomonas campestris pv. vesicatoria,
Salmonella enterica, and YopJ of Yersinia
                                        AvrRxv of Xanthomonas
                                                                                                                                                                                  /product="potential ORFB-specific chaperone'
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                                                                                                                                                                                                                                                                                                                                                                                                                               /product="harpin HrpN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="pathogenic to
<1. .429</pre>
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/strain="Ea246"
                                                                                                                                                                                                                                                transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="hrpN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:552"
                                                                                                                                                                                                                                                                                                              'note="ORFA;
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ce proteins; leucine-rich"
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1079 gccggcaagatcaatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgac 1138

Query Match Best Local Similarity Matches 329; Conserv

Conservative

0;

Score 153.6; DB 1; Pred. No. 5.1e-20; 0; Mismatches 234;

Length 4291; Indels

15;

Gaps

2;

56.9%;

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BASE COUNT
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MLSEMGNNGLDQAITPDGQGGGQIGDNPLKANLKLLARMMCQSDDQFGCPGTGNSSA
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GSELGDGGQSENQKPLFILEDGASLKNVTNGDDGADGIHLYGDAKIDNLHVTNVGGEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2587. .2592) complement(3929. .3934)
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RIQNSEWDCIMYSLNNALKSFKHHDEYTARLHKGEKIPVPAEFFKHAQSKSMVEGLPH
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                                                                                                                                                                                                                                                              4120. .>4291
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/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                          1050. .4080
"note="HrpL-dependent promoter
1105. .×4291
'gene="dspE"
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/protein_id="AAF63401.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctcaacgccaacactcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatg
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/number=2
257. .264
/note="Chi
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218. .225
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/note="minisatellite
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                                                                                                                     /rpt_type=direct
185. .192
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/db_xref="taxon:7226"
                                                  'note="Chi sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MBK20
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.orni.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://cCR-081.mit.edu/GENSCAN.html),
MetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
                                                                                                                                                                                               Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                          Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned Pl and TAC clones DNA Res. 5 (1), 41-54 (1998)
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AB010070 BA000015
AB010070.1 GI:2760166
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389. .396
/note="Chi
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356. .363
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143 c
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Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is T2II and the 3' clone is MXM12.
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LLSCQSWEIMGSFANDTLDLADLEWSDDDSSIVVWDDSPLEYKAYECGLGVKTYSWSPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STAGGSTPEAAGAGAGAAAAGAGAAAAAAAAAAAPGLGAASAGAGAGAGAGTPAPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MFSFLIFLLEVYKVVIAVVASIVFFVFSGLTLAGTAVGLTVTTPLFIFSPILVPATIAITLLTTGFTTGGALGATAIALIRRGMGVKSKNNIPAIGAPPTMFAQFSLTPKINYEGTFKGSWGGKSSPQATPNFSYGGTWTANWGGRSFTGKFGDQSGGG
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FPEMIRTEYYTDRRIYAFSVIGFVKEETDAASYILLHIPNQAVKYNFIDKTFKKLCDF
                                                                                                                                                                                                                                                                                                                             similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                /translation="MGLVEIGGSDAMAAPMOGRVPPPPPPPPPPRPRMPRLPPMFDAFDHT
GAGMYWGFPRPAKKRASIKPHJWKITSDL/GGSLWDEL/ORHGDGQTAIELDISELET
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VDVDQIEKLIKFCPTNEEMELLKTYTGDKAALGKYEQYLLELMKVPRLEAKLRVFSFK
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/db_xref=="01:19759585"
/translation="MCVSTTFWLYCKGLVSEEVIRDESKQIGGFGVAICDHEDNRLYE
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/translation="MCVSTT
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gene_id:MBK20.8"
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/codon_start=1
                                                                TQFGTKITELKERLNVVTSACEEVRSSEKLKEIMKKIPCLGNTSNQGPDRVGVKLDSS
VSDYHTVKSHHYYCKVLASEASELLDVYKDLQSLESAGSIQVRSLAQNIQAIIKKLEK
VSDYHTVKSHHYYCKVLASEASELLDVYKDLQSLESAGSIQVRSLAQNIQAIIKKLEK
LKQELTASEEDGPASEVFCNYTLKDTISIAETEMATVLSLYSVVLJFKKAHEENVKQADL
EKKKAMKQIDLRRANDTEIMLTKVNIPLADMMAAVLGMDEYVLDVDQIENLIRFCPTK
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/protein_id="BAB11443.1"
/db_xref="GI:9759586"
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pir||T17454
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13356. .13447,13592. .13681,13826. .13897,14025. .14162,
14266. .14421,14707. .14845,14945. .15011)
/note="gb|AAD38624.1
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/protein_id="BAB11440.1"
/db_xref="GI:9759583"
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SEMELLKNYTGDKATLGKCEQLAKAKAPLKEHFRVINAFPSLTPQYFLEVMKVPGVES
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/product="tRNA-Leu(CAA)"
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                                                                                                                                                                                                                                                                                                                        Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M. A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G. Deciphering the biology of Mycobacterium tuberculosis from the
   Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcor Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                                                                          Parkhill,
                                                                                                                                                                                                                                                                      complete genome sequence
Nature 393 (6685), 537-544 (1998)
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1 (bases 1 to 47852)
                                                                                                Direct Submission
                                                                                                                                                                                                                 Erratum: [[published erratum appears in Nature 1998 Nov
                                                                                                                                                                                                                                                    98295987
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2 (bases 1 to 47852)
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LKSLAEEIQAITKGLEKLNKQLTASESDGPVSQVFRKVLKDFISMAETQVATVSSLYS
SVGKNADALAHYFGEDPNHYPFEKVTTTLLSFIRLFKKAHEENVKQADLDKNKDAKEA
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/product="SMC-like protein"
/protein_id="BAB11444.1"
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Pred. No. 0.0026;
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                                                                                                                                                                                                                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Notes:
Details of M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiation codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renumbered from the original cosmid submissions but the odesignations are in brackets after the new gene numbers prediction was based on a Hidden Markov Model of TB genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv3494c, (MTV023.01c), len: 564. Unknown Pro-rich protein similar to several Mycobacterium tuberculosis proteins e.g. MTCI28.14 (515 aa), MTCI9H5.28c (516 aa) and (MTV051.09). Has hydrophobic stretch, possibly signal peptide at N-terminus. FASTA scores: 297050/MTCI28_14 (515 aa) opt: 1006 z-score: 582.8 E(): 5.9e-25; 34.3% identity in 559 aa overlap; 297182/MTCY19H5.28 (516 aa) opt: 979 z-score:567.7 E(): 4.1e-24; 33.5% identity in 555 aa overlap. TBparse score is 0.897"
/note="Rv3495c, (MTV023.02c), len: 384. lprN, similar Mycobacterium tuberculosis proteins MTC128.13 (390 aa) MTC119H5.29 (402 aa) and (MTV051.08). Probably lipoprotein, contains possible signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site. FASTA scores:
                                                                                                                                                                                                                                                                                                                                                                                                                            /GL_XTEGE="STTERMI:053539"
/GL_XTEGE="STTERMI:053539"
/translation="MIDRLAKIQLSIFAVITVITLSVMAIFYLRLPATFGIGTYGVSA
/translation="MIDRLAKIQLSIFAVITVITLSVMAIFYLRLPATFGIGTYGVSA
/translation="MIDRLAKIQLSIFAVITVITLSVMAIFYLRLPATFGIGTYRSVS
DFVAGGGLYKNANVTYRGVAVGRVESVGLINPNGVTAHMRLNSGTAIPSNUTATVRSVS
AIGEQYIOLVPPENESSTKLINGFRIOPGNANVPQVSQLIDQAGPFLQAQIRAGGDI
LHEAFIATINGAGPELARLIESARLLVDEANANVPQVSQLIDQAGPFLQAQIRAGGDI
KSLANGLARFFWQLRAADPRLEDTLANAPDAIDEANLPFSGIRRSFPALASLANLGR
VGSLYHKSIEQLLVVFPALFAAIITSAGGVPQDEGAKLDFKIDLHDPPPCMTGFLPPP
LVRSPADESVEREIPROMYCKTAQNDESTVRGARNYPCQEFPGKRAPTVQLCRDPRGYV
PVGTNPWRGPPIPYGTEVTDGRNILPPNKFPYIPPGADPDFGVPIVGPPPPGQVAGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:1773"
/clone="Y13E12"
<1. .47852
                                                                                                                                                                                                                                             complement(1706.
/gene="lprN"
                                                                                                                                                                                                                                                                                                                                  PAPHOPAQPAPPPNDNGPPPFTSWMPPGYPPEPPQVPYPATIPPPPPPEGTGPPPGPAPGPQPQASGPAYTIYDQLSGAFADPAGGTGIFAPGMTGASSAENWVDLMRDPRQL"
complement(1703. .1707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Rv3494c"
/note="Rv3494c"
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complement:
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physical clone"
                                                                                                                                                                                                                    complement(1706. .2860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein Rv3494c"
/protein_id="CAA17731.1"
/db_xref="GI:2924431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mycobacterium
/strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mycobacterium
/strain="H37Rv"
                                                                                                                                                                                                                                                                             /note="possible RBS for
complement(1706. .2860)
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                                                                                                                                                                                        /gene="lprN"
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note="Rv3497c, (MTV023.04c), len: 357. Unknown but Similar Mycobacterium tuberculosis proteins MTCY19H5.31 (481 aa), MTC128.11, (515 aa) and MTV051.06. Hydrophobic region atN-terminus. FASTA scores: Z97182|MTCY19H5_31 (481 aa) opt:611 z-score: 667.7 E(): 1.1e-29; 32.5% identity in 332aa overlap; and Z97050|MTCI28_11 (515 aa) opt: 587 z-score:641.2 E(): 3.3e-28; 30.1% identity in 3335 aa overlap. TBparse score is 0.889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to Mycobacterium tuberculosis proteins MTCI28.12 (530 aa), MTCY19H5.30c (508 aa) (MTV951.07). Hydrophobic region at N-terminus. FASTA scores: 297050|MTCI28_12 (530 aa) opt:838 z-score: 711.0 E(): 4.3e-32; 35.1% identity in 473 aaoverlap; and 297182|MTCY19H5_30 (508 aa) opt: 821 z-score:697.0 E(): 2.6e-31; 35.1% identity in 453 aa overlap.TBparse score is 0.891"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2857. .4212)
/gene="Rv3496c"
complement(2857. .4212)
/gene="Rv3496c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2867..2871)
/gene="Rv3496c"
/note="possible RBS for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPLGAAINQAADTLDGNGDSLHNALRELAQVAGRLGDSRGDIFGTVKNLQVLVDALSE
SDEQIVQFAGHVASVSQVLADSSANLDQTLGTLNQALSDIRGFLRENNSTLIETVNQL
NDFAQTLSDQSENIEQVLHVAGPGITNFYNIYDPAQGTLNGLLSIPNFANPVQFICGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mnriwlraliltassallagcqfgglnslplpgtaghgegaysv
TVEMADVATLPQNSPVWDDVTVGSVAGIVAVQRDDGSSTARVKIDLDXNVLLPANAV
AKVSQTSLLGSLHVELAPPTDRPPTGRLVDGSRITEANTDRFPTTEEVFSALGVVVNK
GNVGALEEIIDETHQAYAGRQAQFVNLVPRLAELTAGLNRQVHDIIDALDGLNRVSAI
GNVGALEEIIDETHQAYAGRQAQFVNLVPRLAELTAGLNRQVHDIIDALGETKVDFGEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4209. .5282)
/gene="Rv3497c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv3497c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:053541"
/translation="MMGRVAMLTGSRGLRYATVIALVAALVGGVYVLSSTGNKRTIVG
/translation="MMGRVAMLTGSRGLRYATVIALVAALVGGVYVLSSTGNKRTIVG
YFTSANGLYPGDQVRYLGYPYGGIBLEPRSSDVKITMSVSKDVKVPYDVQAVLMSPN
LVAARFIQLTPVYTGGAVLPDNGRIDLDRTAVPVEWDEVKEGLTRLAADLSPAAGELQ
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TFFTTAYFDPNMAHMDEILNPPDFLIGELANLSGQAADPFKIPPGTASGQ"
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/product="lprN"
/protein_id="caA17732.1"
/db_xref="GI:2924432"
/db_xref="SPTREMBL:053540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gp|Z97050|MTCI28_13 (390 aa) opt:653 z-score: 762.1 E
0; 33.6% identity in 363 aa overlap; and
Z97182|MTCY19H5_29 (402 aa) opt: 572 z-score: 667.9 E
1.1e-29; 31_8% identity in 362 aa overlap. TBparse
                                                                                             /product="hypothetical protein
/protein_id="CAA17734.1"
/db_xref="GI:2924434"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATEAKSETPVPELTWVPAGGGAPVGNPADLQSLLVPPAPGPAPAPPAPGAGPGEHGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFDTAAGPSAPDYYRRAEICRERLGPVLRRLTVNYPPIMFHPLNTITAYKGQIIYDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein
/protein_id="CAA17733.1"
/db_xref="GI:2924433"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2798. .2830)
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                        KTYDAYFTDAGGITPGNSVYVSGLKVGAVSAVSLAGNSAKVTFSVDRSIVVGDQSLAA
                                                                                                                                                                                /transl_table=11
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                                                                             db_xref="SPTREMBL:053542"
                                                                                                                                                                                                        codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="PS00013 Prokaryotic
                                                translation="MLNRKPSSKHERDPLRTGIFGLVLVICVVLIAFGYSGLPFWPQG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rv3495c"
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Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCGACCGCTACCGGTGCCACCGGCGCACCGGGTTTTCCGGTGGAGCCGGCGGGCCG 20948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cggccgatagcgggggcggcggtacaccggatgcgacaggtggcggcggcggtgatacgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGCGGCGCGGCGCGCGGTGGTGCTGGCGGTGTCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGGGCCGGCGAACACCGGGGTTGGCGGCCACCAACGGCTCCGGCGGGCAAGGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cctcaggtactggctcggtgtcggacaccgcaggttctaccgagcaagccggcaagatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGTATCGGCGGCACCGGCGGCCAAGGCGCGGCGGCGGCGGCAGCGCCAGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcggtggcgagggtggcgtaacaccgcaaatcactccgcagttggccaaccctaaccgta 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtggcggcggcacacccactgcaacaggtggcggcagcggtggcacacccactgcaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCGGGATTGGCGCCGACGGCGGCGCGGGTGGGACTGGCGGTAACGCCGGCGCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caagcgcaacaggcggtggcggtgatactccgaccgcaacaggcggtggcggcagcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCCGGCGGGCCCGGCACCGGAGGAACCGGCGGGGTTGTCGGCGCCGCGGGCAAGG
Streptomyces
                                                          histidine kinase; two component system response uracil DNA glycosylase.
                                                                                                              ABC transporter ATP-binding protein; ABC transporter transmembrane protein; asnC-family transcriptional regulatory protein; hydrolase; integral membrane protein; lipoprotein; mark-family transcriptional regulator; oxidoreductase; oxidoreductase, iron-sulphur binding subunit; oxidoreductase, molybdopterin binding subunit; regulatory protein; secreted deacetylase; secreted lyase; secreted protein; tetR-family transcriptional regulator; two component system
                                                                                                                                                                                                                                                                                                                                                                                                          SC2G38 4
Streptomyces
                                                                                                                                                                                                                                                                                                                                            AL445503.1 GI:10803131
                             Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNVFTQALHDATPQVRGAVDGLTSLSRALNRRDEALQGLLAHAKSVTSVLSERAEQVN
KLVEDGNQLFAALDARRAALSALISGIDDVAAQISGFVADNRKEFGPALSKLNLVLAN
LNERRDYITEALKRLPTYATTLGEVVGSGPGFNVNVYSVLPGPLVATVFDLVFQPGKL
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/protein_id="CAA17735.1"
/db_xref="GI:2924435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5272. .6324)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Rv3498c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                          40549 bp
s coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.7%;
                                coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64.4; DB 3;
Pred. No. 0.0054;
D; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                             cosmid 2G38
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              BCT
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                                                                                           regulator; ung,
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JOURNAL REFERENCE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                 CDS
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The more
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Submitted (13-OCT-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, (3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13pb before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinashi,H. and Hopwood,D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     upstream initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overlap between neighbouring submissions. Cosmid 2G38
                                                                                                                              /Clone="cosmid 2G38"
complement(1. .320)
/gene="2SCG38.01c"
complement(21. .320)
/gene="2SCG38.01c"
/note="2SCG38.01c, possible regulatory protein(fragment),
/note="2SCG38.01c, possible regulatory protein(fragment),
len: >106 aa; similar to N-terminal region of TR:CAC01635
(EMBL:AL391072) Streptomyces coelicolor putative
regulatory protein SC9A4.08, 116 aa; fasta scores: opt:
218 z-score: 308.8 E(): 9.3e-10; 46.28 identity in 91 aa
/product="putative regulatory protein(fragment)"
                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces coelicolor A3(2)"
/strain="%3'2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptomyces
/db_xref="taxon:1902"
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gene
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1739. .2530
                                                                                                                                                                                                                                                                                                          complement(2544. 3350)

/gene="2SCG38.04c"
/note="2SCG38.04c, conserved hypothetical protein, len:
/note="2SCG38.04c, conserved hypothetical protein, len:
268 aa; similar to TR:053782 (EMBL:AL021943) Mycobacter;
tuberculosis hypothetical 26.5 kDa protein MTV040.02, 24
aa; fasta scores: opt: 735 z-score: 848.5 E(): 0; 51.48
identity in 218 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative secreted lyase"
/protein_id="CAC13062.1"
/protein_id="CAC13062.1"
/db_xref="G1:10803134"
/translation="MTAVTRPRARRAVTGALGALGLSVGMLMTSGASSAQAATWPTPN
/translation="MTAVTRPRARRAVTGALGALGLSVGMLMTSGASSAQAATWPTPN
GSEGVSSTLSVSGTKDYGMKRLYGTGDLGSGGGDEDGCFILELAFGAVLKNVIIGAAPA
ADGVHCKGSCTLQNVWMEDVGEDAATTPRGSSSGVDTDVGGGAKEADDXKNVFTOFNGAGT
LNISGFAVKNFGTFVRSCGNCSTQYRRTINLNGIEVNWKGGRIAGINTNYGDSATLRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="2SCG38.03, probable secreted lyase, len: 266 aa; similar to TR:Q04701 (EMBL:M94691) Fusarium solani pectate lyase A precursor (EC 4.2.2.) PelA, 242 aa; fasta scores: opt: 605 z score: 664.1 E()::1.69-29; 43.68 identity in the content of th
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DAVREVWPDDKPLFFRVSATDWLEEGGWTPDDTVRFARDLEAHGIDLLDVSTGGNVPR
VRIPTGPGYQVPFAARVKAGSTLPVAAVGLITEPGQAEKILANGEADAVLLGRELLRN
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/protein_id="CAC13061.1"
/db_xref="G1:10803133"
/db_xref="G1:10803133"
/td_xref="G1:10803133"
/tanslation="MSALFEPPRLRDTTIPNRIMMPPMCQYSAAPEGPSAGVPGDWHF
AHYGARAVGGTGLIVVEATGVSPEGRISPQDLGLWNDTQVEAFRRITGFLRSQGTVPA
VQLAHAGRKASTAQPWRGGAPVGADAYGWQPLAPSALAFDERHPVPTELTVPQIQEAV
                                             /product="conserved hypothetical
/protein_id="CAC13063.1"
/db_xref="GI:10803135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="2SCG38.04c"
complement/25'
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/codon_start=1
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/db_xref="GI:10803132"
/tanslation="MyPBAATAAGTRELPHPTRAEIRLEGVLHALSDPVRLRIVRDLAA
/translation="MyPBATAAGTRELPHPTRAEIRLEGVLHALSDPVRLRIVRDLAD
DSGALFSCSHFDLPVTKSTTTYHFRVLRESGVIRQTVRGTAKMNGLRRDDLDIVFPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITIVGDSSKKIVPCQKYIGNDDGDEPDSNGSGADGTYCKYSSSDITYK"
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translation="MGARTVRAHVDERRGAARMTGSGDPGRLTLRPLSARSVILSLLL/
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tg---agcatcgagctgaacggcatcgaagctaac 1564
| | | |||| | || |||||||||||||
                                                        TCGCCGTCAAGAACTTCGGCACCTTCGTCCGGTCCTGCGGCAACTGCTCGACGCAGTACA
                                                                                          tcaaggccgacgatttcggcacgatggttcgcaccaacggtggcaagcagtttgatgaca 1532
                                                                                                                                                                          CCTTCCGGGGCTCGTCGTCGAACGTC-----TACACCGTCTCCGGCGGCGCCGCCA
                                                                                                                                                                                                                                                        cggtcaaaggcgagggaggcgcagcggtcactaatctgaacatcaagaacagcagtgcca 1412
                                                                                                                                                                                                                                                                                                       GCACGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCTCCGGCGGCCAGGACGAGGACCAGGGCCCGATCCTGGAACTGGCTCCCGGCGCCC 2012
                                                                                                                                      AGGAGGCCGACGACAAGGTGTTCCAGTTCAACGGCGCCGGAACGCTGAACATCTCCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to dehydrogenase, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAVPALRAQPELAEVYEPLLTSREYEPGLRTPTDKRGLLAGMGMTEKQGGSDVRTNAT
TATATAEPGYYTLRHKWFTSAPMCDVFLVLAQAAGGLSCFLVPRVLPDGTRRTFRVQ
RLKDKLGNRSNASSEPEFDGTVAMLVGPEGQGVKTIIEMVNCTRLDCVMASATLMRKT
LVEAGHHVRHRTAFGARLVDQPLMRNVLADLALESEAATALTLRLAGAADRAVRGDEG
EAAFRIATAYGKYWYTKRGPAFTAEALECLGGNGYVEESGMERHYREAPLLSIWEGS
GNVNALDVLRALGRSPAAAQALFGELSLARGADARLDAAADRLRTGLTEASETGARRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTTLAQEPPYESYEPSEEPWGRPEGYATHDVTNQPPPLAPYDAS
DDTVLLEGLRREGAGWAEDGLRRLGRRAGSAQAQDWGDLANRHEPVLRTHDRYGNRVD
EVEYHPSWHHLMRVAVGEGLAGAPWADGRPGAHVARTAGGLVWGHTEAGHGCPTSMTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="25CG38.05, probable oxidoreductase, len: 567 as similar to SW:ALDB_ECOLI (EMBL:120915) Escherichia col oxidoreductase AidB protein, 541 aa; fasta scores: opt 1437 z-score: 1553.6 E(): 0; 45.8% identity in 517 aa
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QDEALRPHTRAWDGDWETLVITATGRDPAARAELRTRLAALRLAELREGVWLRPANLD
RPLPTDLGRVAERLVSRPGSPAVELAARLWPLVDWADTARALLVHVDRARRPAGLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to dehydrogenase, score
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/protein_id="CAC13064.1"
/db_xref="g1:10803136"
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Pred. No. 0.015;
0; Mismatches 163;
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2.10, E-value 8.7"
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Robinson,C., Rivolta,C., Karamata,D. and M
The product of the yvoC (gerF) gene of Bac
required for spore germination
Microbiology 144 (Pt 11), 3105-3109 (1998)
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Stulke,J., Karamata,D., Saier,M.H. Jr. and Hillen,W
A novel protein kinase that controls carbon catabol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-AUG-1997) IGBM, Switzerland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 47739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 47739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 30303 to 37035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiol. 27 (6), 1157-1169 (1998)
                                                                                                      /gene="yvjA"
1350. .2195
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                                                                                                                                                                                                                                                                                                                                                          KVETLDYLPGDEAGIKSVTLLIKGHNAYGYLKAEKGVHRLVRISPFDSSGRRHTSFVS
CEVMPEFNDEIDIDIRTEDIKVDTYRASGAGGQHVNTTDSAVRITHLPTNVVVTCQTE
RSQIKNRERAMKMLKAKLYQRRIEEQQAELDEIRGEQKEIGWGSQIRSYVFHPYSMVK
/note-"similar to thermophilic bacterium PS-3 hypothe protein: PIR Accession Number S43727 and to Bacillus subtilis xqfU, xpjC and YitB proteins" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="melseiraelenmasrladfrgsldleskeariaeldeqmadpe
fwndqqkaqtvineanglkdyvnsykklnesheelqmthdlikeepdtdlqlelekel
ksltkefnefelqlllsepydknnailelhpgaggtesqdwgsmllrwytrwgerrgf
                                                                                                                                                                                                                                                                                                                           DHRTNTEMGNVQAVMDGDIDTFIDAYLRSKLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative peptide chain
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                                                                                                                                                                                           /gene="yvjA"
1338. .2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UGAC) are translated as Asp,
20, 4423-4428, 1992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="at low concentrations of RF-2 nucleotides 155. (UGAC) are translated as Asp, Pel,H.J. Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="prfB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bacillus subtilis"
/db_xref="taxon:1423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="prfB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           map="300-304 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to 47739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "prfB"
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300-304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .154,156. .1184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karamata, D. and Moir, A. (gerf) gene of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degree genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                release
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/transl_table=11
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2244. 250
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2816. .3502
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3495. .4385
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2806. .3502
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LNLNNAATNAEKQVEIKVLIDLTADQKAQDKLQNDIKELKGIGSVTESSKEKELDQLV
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LFKVVGVSRNIGIALIIGLVFTAMFLISNTIKITIFARKEIELMKLVQATNWFIRWP
FFLEGILLGVFGSVIFIALVLSTYQYVIGWVVPKVQGSFVSLLPYNPFVFQVSLVLIA
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ADEPTGNLDPDTSWEVMKTLEEINNRGTTVVMATHNKEIVNIMKKRVIAIEDGIIVRD
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FSDSLDSSFEGIGAEVGMEDGKIIIVSPFKKSPAEKAGLKPNDEIISINGESMAGKDL
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EELYQQSCVGCHGKDLEGVSGPNLQEVGGKYDEHKIESIIKNGRGNMPKGLVDDNEAA
                                                                                                                                                                                                                                                                                                                                                                         [GAVIGVWGSLTSIRKFLRV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="cytochrome c-551"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="cccB"
2223. .2582
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IVVTAMIVENIEQGLYAMLGVYVSSKTIDVVQVGFNRSKMALIITKQEQAVKEAVLQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=experimental
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Best Local
   37514
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                                            gttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcga 1269
TTTTCGTGTGGAGGATGGAGCAACCCTGAAAAATGTGGTGCTTGGTGCACCTGCAGCTGA 37455
                                                                                                                                                                     aaccttcactgccgacaaatctatgggtaacggagaccagggggaaaatcagaagcccat 1209
                                                                                                                                                                                                                                                                  CAAAGTGGTGCACGAAACAATTATCGTACCAAAAAATACAACATATGACGGGAAAGGACA 37575
                                                                                                                                                                                                                                                                                                        caatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgc 1149
||| |||||| | | | | | | | | |
                                                                                                                                   GCGGTTTGTGGCAGGGAAAGAATTAGGTGACGGAAGCCAGTCAGAAAACCAAGACCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="belongs
regulators"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(9366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8025 .9373)
/gene="yvkA"
complement(8025 .9359)
/gene="yvkA"
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/product="T2"
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6784. .7977
/gene="yvjD"
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6773...6
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6784...
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ISTFSEITABDFAKALRELEKKEIEGLVIDVRCNPGGVLQSVEELIKHFVTKDQFYIQ
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GTVQQAVPMGDGSNIKLTLYKWLTPNGNWIHKKGIEPTIAIKQPDYFSAGPLQLKEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="9959"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt RYFGSIISSALIGLISGYHTLFMILFAVSIIGVFVSLGIKSDETARIEKNSA"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VASGS"
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6773. .7977
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                 3.3%;
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.6777
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                                                                                                                                                                                                                                                                                                                                                                                              Score 57.6; DB Pred. No. 0.11; 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the TetR/AcrR family of transcriptional
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                                                                                                                                                                                                                                                                                                                                                               Foulger, D. Filtz, C., Fujlta, M., Fujlta, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S. Y., Glaser, P., Goffeau, A., Golightly, E. J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Grandi, G., Guiseppi, G., Guy, B.J., Hasono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Kalerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Kningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Schowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Schowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Soldo, B., Soldo, B., Takadain, H., Takahashi, H., Takemaru, K., Takadano, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vasamotti, A., Vannier, F., Vasamotti, A., Voshikawa, H. F., Zumstein, F., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cggtgg 1515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACGATCGACGGCGGTTCTGCTCAAAAAGCGTCAGATAAGATATTCCAAATCAATAAAGC 37302
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Submitted (18-NOV-1997) I. Moszer, A. Regulation de l'Expression Genetique,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entland, K.D., Errington, J., Fabret, C., Ferrari, E., Foulder, D., Fritz, C., Ferrari, E., Foulder, D., Foulder, D., Fritz, C., Ferrari, E., Foulder, D., Fritz, F., Foulder, D., Fritz, C., Ferrari, E., Foulder, D., Fritz, C., Ferrari, E., Foulder, D., Fritz, C., Ferrari, F., Foulder, D., Foulder, D., Fritz, C., Ferrari, F., Foulder, D., Foulder, D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 209510)
Kunst.F., Ogasawara.N., Moszer.I., Albertini, A.M., Alloni, G.,
                                                                       Direct Submission
                                                                                                       Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
                                                                                                                                                                                                                                                Bacillus subtilis
                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                             Yoshida, K., Yoshikawa, H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
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                                                                                                                                           (bases 1 to 209510)
                                                                                                                                                                                                                                                                            complete genome sequence of the
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                                                                                                                                                                                                        249-256 (1997)
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                                                                                                                                                                                                                                                                                                                                                Zumstein, E.,
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                                                                                                                                                                                                                                                                            gram-positive bacterium
   Danchin, Institut Pasteur, 28 rue du Docteur Roux, 75724
                                                                                                                                                                                                                                                                                                                                                Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AAAGT 37362
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adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, F
68 89 48
                                                                                                                                                                                                                                                                                                                                                complement(3001.
                                                                                                                                                                                                                                                                                                                                                                                 GAPVFALILIRQHRGGRSL"
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                                   /protein_id="CAB15323.1"
/db_xref="GI:2635831"
                                                                                                                                                                                                                                                                            complement(3001. .3945)
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/protein_id="CAB15322.1"
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/db_xref="GI:2635829"
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/protein_id="CAB15320.1"
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/strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                            'gene="yvrC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:2635830"
/db_xref="SPTREMBL:034451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="yvrB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="yvrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="yvrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yvqK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="yvqK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1423"
                                                                                                                                           codon_start=1
                                                                                                                                                                               note="similar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="GI:2635828"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="yvqK"
       db_xref="SPTREMBL:034805"
                                                                                                                                                                                                               function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function="unknown"
                                                                                                                                                                           δ
                                                                                                                                                                           iron-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKVLGDGGGTGDILIAATQTQQSENIEQRLNQLIKKGTAECIKEAAELFE"
                                                                                                                                                                                                                                                                                                                                                FLLGTILLIINGRELNYMTYGEDKAKLLGVSVQQRKMMILIAGSLLTGSAVAVSGTIG
FVGLVIPHITRLLWGTDHRHLLPLSALLGAGFLVLADLLSRTIIEPIELPIGIITSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMSVSTLILTGVITNSFLGAFISLIIALTGDNLLPIVHWLLGSVSMRGWSYVILFLPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDILLQTEIPLRTLSSTPIGAGFSWSRTLIHKRLPDQPDPIEGLTACLSESGFQLQET
CAMASSERLDRFVYRTYEDGELSVFICVQTGFSIWILINGYAADQFFIKALMAAEAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAGARVVNARSGIGDVEYERSAIVFRDRNSSES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAPELKKFILPGGSKCASLLHIARTITRRAERRVVALMKSEEIHETVLRYLNRLSDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to iron permease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MKLYTKTGDKGQTGLVGGRTDKDSLRVESYGTIDELNSFIGLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="similar to iron transport system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical proteins"
protein"
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DTLEAYLDVNEDGTWEVDNFLKKSVDKQHGWMQIIDSEGNTDYSYGVPKDVPGTYTKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB15324.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVNVEKVISLKPDLVLAHESSMSASADAIKQLKDAGITVLTVNDAQSFSEVYKSIEMI
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NEMLNVIHAKNAAADQTGWVQMTDEAIVKLNPDAIVTTDGVKAKAVEKRDGWSEINAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LISLSRGMAEMTKGTNVTVNSVLPGPTWTEGVASYMEGAAQAAGQDTDTFIKDYFKVN
EPTSLIQRYATAEEVANTIVFLASDAASAINGTAQRVEGGIIRSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mkkragiwaalllaavmlagcgnpadqkdskakqktevfpvtid
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KGMDEETITHLFNRYYRGTNTKDSTAGTGLGLAIAKELVHLHNGTIHVNSRTNIGTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6122. .7843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLETGGYQPVPFAGDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5172. .6050)
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                                                                                                                         complement(7861. .8970)
                                                                                                                                                                           complement(7861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB15326.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6122. .7843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5172. .6050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEEWNQYFEVNVMSAVRTSRHFLPKMLAKNSGRILNIASEAGVKPLPTMIPYSMTKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHHRVYDVDPDLVTRSGPRLIEGVEELAESIYPDTFKE"
                                                                                                                                                 /gene="yvrH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MFHFFGQMLIVILLLTVMLVASFFYLDARFSDAESNSGLTKATT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [YvrH]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="yvrG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="yvrE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yvrD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yvrD"
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                                                                         function-"unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="yvrG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                          codon_start=1/
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                                                  to two-component response regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to two-component sensor histidine kinase
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                                                  [YvrG]"
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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KEYWORDS
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FEATURES
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Query Match
Best Local Similarity
Matches 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1090 caatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgc 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cggtgg 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTACCTTCACAGTGAAAAATTTCACGGCGGATAATGGCGGGAAGTTCATTAGACAGCT 190591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGATCGACGGCGGTTCTGCTCAAAAAGCGTCAGATAAGATATTCCAAATCAATAAAGC 190531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaacatcaagaacagcagtgccaaaggtgcagacgacaaggttgtccagctcaacgccaa 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcga 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaccttcactgccgacaaatctatgggtaacgggagaccaggggcgaaaatcagaagcccat 1209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cactcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatggttcgcaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTCGTGTGGAGGATGGAGCAACCCTGAAAAATGTGGTGCTTGGTGCACCTGCAGCTGA
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                                                                                                                        PR
PI KOICHI MIZUNO, TOMOHIKO KATO, SHIGERU SATO, DAISUKE SHIBATA CLI2N15/09, A01H5/00, C07K16/40, C12N5/10, C12N9/10, C12P21/02// PC (C12N15/09, C12R1:91), (C12N5/10, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,
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Vigna angularis
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
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E32986
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Koichi, M.T.K.K. and Sato, D.S.
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                                                                                                  C12N5/00, (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
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Search completed: October 4, 2001, 22:26:29 Job time: 7060 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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SUMMARIES

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ALIGNMENTS

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WPI; 1999-167125/14. P-PSDB; AAW97851.	Alfano JR, Charkowski A, Collmer A;	(CORR) CORNELL RES FOUND INC.	06-AUG-1997; 97US-0055107.	24-JUL-1998; 98WO-US15501.	18-FEB-1999.	WO9907207-A1.	/*tag= a	CDS 4191693		Pseudomonas syringae pv. tomato.		Hypersensitive response elicitor; dspE gene; HrpW; transqenic plant; disease resistance; insect resistance; ss.	Hypersensitive response elicitor HrpW dspE gene.	07-JUN-1999 (first entry)		RESULT 1 AAX24347 ID AAX24347 standard; DNA; 1729 BP.

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New hypersensitive response eliciting (dspE) gene and protein useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
Claim 1; Page 37-38; 56pp; English.
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This the DNA sequence of the dspE gene of Pseudomonas syringae pv tomato DC3000 that codes for a 42.9 kDa hypersensitive response celicitor (HRE) polypeptide (see AAW97851), termed HrpW. To identify any HRE-like genes in the P. syringae pv. tomato DS3000 DNA flanking hrpR, cosmid pCPP2357, which contains this region in vector pCPP47, was isolated. A series of subclones in pML123 were constructed and Screened for 2 potential HR phenotypes: (1) the ability to promote tobacco HRE activity in Pseudomonas fluorescens cells carrying pCPP274, a delhrp2 pHT711 derivative, and (ii) interference with CC pCPP2774, a delhrp2 pHT711 derivative, and (ii) interference with CC pCPP2774, a delhrp2 pHT711 derivative, and (ii) interference with CC pCPP2774, a delhrp2 pHT711 derivative, and (ii) interference with CC pCPP2773, had the first phenotype, but one, pCPP2373, had the CC second. Transcriptional unit v of this subclone contained the CC second. Transcriptional unit v of this subclone contained the CC second. Transcriptional unit v of this subclone contained the CC second. Transcriptional unit v of this subclone contained the CC second. Transcriptional unit v of this subclone contained the CC second. Transcriptional unit v of this subclone contained the CC second. Transcriptional unit v of this protein or contained DNA molecule can be used to impart disease resistance to CC plants. This is achieved by applying the HRE protein in a CC con-infectious form to plants or plant seeds. Alternatively, CC transgenic plants or plant seeds. Alternatively, CC transgenic plants or plant seeds transformed with DNA encoding the CC contained the CC contained transcriptional seeds transformed with DNA encoding the CC contained the CC contained transcriptional contained transcriptional contained transcriptions.

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Best Local Similarity
Matches 330; Conserv
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                                                                   The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a DNA encoding hypersensitive
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                                 response elicitor protein from Erwinia amylovora. The protein is heat stable, protease sensitive and suppressed by inhibitors of pretabolism. The present sequence is used to transform transgenic
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Sequence 1344 BP;
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                                                                                                                                             Application of a hypersensitive response elicitor protein to plants impart stress resistance -
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/product= "Hypersensitive response elicitor"
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343
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                        stress resistance.
372 C;
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Query Match
Best Local Similarity
Matches 330; Conserv

Conservative

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Score 155.2; Pred. No. 8.3e 0; Mismatches

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                                    05-OCT-1998;
                                                                                                                                                                                                         Erwinia
                                                                                                                                                                                                                                   ornamental plant;
                                                                                                                                                                                                                                              Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; c
                                                                                                                                                                                                                                                                                    DNA encoding a hypersensitive response elicitor protein
                                                                                                                                                                                                                                                                                                              08-AUG-2000
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  1270
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hes 330;
agtgatatctcactgggtgatgttgaaaaccactacaa 1307
                         ggcaacatcgccatgaccgacgtcaaacacgcctacga 1656
                                                                                                                                                                                  gttcgcaccaacggtggcaagcagtttgatgacatgagcatcgagctgaacggcatcgaa 1558
                                                                                                                                                                                                                                                                                  ctcaacgccaacactcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatg
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                                                                            gcagaagacggtaagttctcgttcgttaaaagcgatagcgaggggctaaacgtcaatacc
                                                                                                 gctaaccacggcaagttcgccctggtgaaaagcgacagtgacgatctgaagctggcaacg 1618
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Pred. No. 8.3e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1154
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P-PSDB; AAW77412.
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09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity, and can be produced on a mass scale.
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tttcgtctggaggctggggcaagcctgaaaaatgtagtgattggcgctcctgccgctgac
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Pred. No. 2.3e-05;
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                                                                                                                                                                    This sequence represents a gene encoding a subunit of the cellulose synthates complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
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                                                                                                                                              Sequence 10732 BP; 3149 A; 1212 C; 2074 G;
                                                                                                                                                                                                                                                                Claim 2; Page 14-21; 32pp; Japanese
                                                                                                                                                                                                                                                                                       A gene encoding a cellulose synthetic equipment - for the improvement in the amount of cellulose synthesised in a plant body
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(OJIP ) OJI PAPER
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                                                                              h 3.3%; Score 57; DB 21; Similarity 13.4%; Pred. No. 0.00015; 55; Conservative 451; Mismatches 525
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                                                                                                                                                                                                                                                                                                AAQ21833
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 173; Conserv
   1496
                                                                                                                                                       1316
                                                                                                                                                                                                                                                                                                                 The sequence is that of an example randomising oligonucleotide which is used in the prepn. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone action and as catalysts. See also AAQ21830-Q21832.
                                                                                                       1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New method of systematic polypeptide evolution by reverse translation - by linking each polypeptide in sample mixt individualised mRNA allowing further synthesis of selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ21833 standard; DNA; 390
                                                                                                                                                                                                                                                                                               Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 55; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-080018/10.
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atggttcgcaccaacggtggcaagcagtttgatgacatgagcatcgagctgaacggcatc 1555
                                                                                                                                            gagaacgaggtcgatggcatccacgtgaaagcccaaaaacgctcaggaagtcaccattgac
                                         cagctcaacgccaacactcacttgaaaatcgacaacttcaaggccgacgatttcggcacg 1495
                                                                                          gcggtcactaatctgaacatcaagaacagcagtgccaaaggtgcagacgacaaggttgtc 1435
                                                                                                                            binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuerk
                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                 194; Indels
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Query Match
Best Local Similarity
Matches 173; Conserv

Conservative

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Indels Length

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390; 0

3.3%;

Score 56.6; DB 14; Pred. No. 5e-05; Mismatches

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RESULT 1
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ID AAQ3
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                                                                                                                              SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune mice which are the fl progeny of a cross of NZB and NZW parents (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone H2B protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a T7 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes.
                          terminating in a restriction endonuclease site is synthesised and cloned using a number of oligonucleotides (example shown). A 3' fixed sequence is placed into a restriction site to provide an mRNA encoding the C-terminal trailer sequence of ca. 100 nucleotides lacking stop codons. In addition, a 3' primer annealing site is provided so that cDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also AAQ36845-63.
Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                              Systematic
                                                                                                                                                                                                                                                                                                                                                                                        Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Systematic peptide evolution by reverse translation; specific; inhibitors; probes; assay; cell sorting; ss
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                                                                                                                                                                                                                                                                   Example 1; Page 84; 98pp; English.
                                                                                                                                                                                                                                                                                                   molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                         Pribnow D,
                                                                                                                                                                                                                                                                                                                polypeptide evolution of polypeptide ligand
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                                                                                                                                                                                                                                                                                                                by reverse translation - used specific for desired target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPERT; ligand;
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RESULT 1
AAF76910
ID AAF76910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-1992;
02-AUG-1990;
01-AUG-1991;
                 The present sequence was used in an example illustrating an invention relating to a method for isolating a polypeptide ligand for a desired target molecule. The method involves synthesising a nucleic acid mixture comprising mRNA having translatable and non-translatable regions and a mixture of nucleic acid polypeptide copolymers, each comprising the mRNA and a cold polypeptide copolymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (PRIB/)
(SMIT/)
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                                                                                                                                                                      Example; Column 39;
                                                                                                                                                                                                                              Isolating a polypeptide ligand to a target molecule, useful for diagnostic assays, comprises partitioning candidate mixtures con of ribosome complexes or mRNA.polypeptide copolymers relative ty affinity to the target molecule.
                                                                                                                                                                                                                                                                                                                                             WPI; 2001-243412/25
                                                                                                                                                                                                                                                                                                                                                                                             Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GOLD/)
(TUER/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence containing a 120 repeat of ACG flanked by fixed fragments.
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TUERK C.
PRIBNOW D.
SMITH J D.
                                                                                                                                                                                                                    ៩
                                                                                                                                                                                                                                                                                                                                                                                          Tuerk C,
                                                                                                                                                                                                                 the target molecule
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90US-0561968.
91US-0739055.
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                                                                                                                                                                                                                                                                                                                                                                                             Pribnow
                                                                                                                                                                 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide evolution by reverse translation;
     its associated mRNA.
                                                                                                                                                                                                                                                                                                                                                                                             Smith
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The copolymers
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RESULT 1
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Best Local S
Matches 173
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                                                                                                        CDS
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                                                                                                                                                Bacillus
                                                                                                                                                                        cellulase; protease; bleaching agent;
                                                                                                                                                                                      Bacillus sp. strain KSM-P15; pectic acid lyase; protopectinase;
protopectin; polygalacturonic acid; detergent; cotton; surfactant;
                                                                                                                                                                                                                             Bacillus sp strain KSM-P15 pectic acid lyase encoding
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1..591
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Pred. No. 5e-05;
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08-APR-1998;

98WO-JP01613

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detergent composition containing protopectinase active at alkaline pH - on protopectin and polygalacturonic acid, provides better removal of muddy soil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hatada Y,
Shikata S,
                                                      AAX89484 standard;
                                                                                                                                                                                                                                                                                                                                                                      1271
                                                                                                                                                                                                                                                                                                                                                                                                                           1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a protopectinase having an optimum pH 7 or higher against protopectin and polygalacturonic acid substrates. Inclusion of protopectinase gives a composition that provides better removal of muddy soil, particularly from socks. The present sequence encodes pectic acid lyase from Bacillus sp. strain KSM-P15, which is used in an example from
17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-568339/48.
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09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 71-72; 80pp; English.
                                                                                                                         403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention. Pectic acid lyase exhibits protopectinase
                                                                                                                                     ggtggcaagcagtttgatgacatgagcatcgagctgaacggcatc 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t---tcactgccgacaaatctatgggtaacggagaccagggcgaaaatcagaagcccatg 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggaggcaccacctacaaagtggtgatgaacgtggaaaactgcaac 447
                                                                                                                                                                                         actcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatggttcgcaccaac 1510
                                                                                                                                                                                                                                                          aacatcaagaacagcagtgccaaaggtgcagacgacaaggttgtccagctcaacgccaac
                                                                                                                                                                                                                                                                                                     ggcatccacgtgaaagccaaaacgctcaggaagtcaccattgacaacgtgcatgcccag 1330
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                                                                                                                                                                          gggacgatcaacattcgtaacttcagggccgatgacatcgggaagctggttcggcagaac
                                                                                                                                                                                                                                aacatctcgggcggggcagcctacaaggcgtatgacaaggtgttccaaatcaatgcagcg
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Suzumatsu
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(first entry)
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97JP-0091142.
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tsu A,
                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3%;
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Tsumadori M,
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Pred.
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Wada
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da Y;
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                                                                                                                                                                                                                               The present sequence is a DNA encoding pectate lyase I. It is a pectin degrading enzyme derived from Bacillus licheniformis, ATCC 14580. The enzyme comprises a catalytic active domain and a cellulose binding domain (CBD) that are operably linked to each other. It shows optimum activity at pH greater than 9 and temperature 55 degree centigrade. It can be used in detergent compositions, for cleaning hard surfaces, for machine treatment of fabrics, for improving the properties of cellulosic fibres, yarn, woven or non-woven fabric, for the degradation of plant material e.g. recycled waste paper, mechanical paper-making pulps or fibres subjected to retting process, for preparing animal feed and for processing wine or juice. DNA encoding the enzyme can also be used for the production of transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pectate lyase I; EC 4.2.2; pectin degrading enzyme; ATCC 14580; catalytic activity; pH; detergent composition; yarn; cellulosic fibre; recycled waste paper; pulp; retting process; animal feed; wine; juice;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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06-MAY-1998;
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                                                                                                                                                                                                                             Sequence 666 BP; 205 A; 136 C; 178 G; 147
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                                           147
                                                                                                  87
                                                                                                                                                                      Local Similarity
gttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcga
                                                                                                               caatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgc 1149
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DB; AAY28446.
                                                       aaccttcactgccgacaaatctatgggtaacggagaccagggcgaaaatcagaagcccat 1209
                                        gcggctgattgcaggtccggagctcggggacggcagccaacgcgaggatcaaaaaccgat
                                                                                               cgaggtcgttcacaaaacgatcgtagtcgagaaaggccaaacgtatgacggaaaaggcaa 146
                                                                                                                                                       154;
                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Page
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                                                                                                                                                         Conservative
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98US-0073684.
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                                                                                                                                                       0;
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                                                                                                                                                       Score 55.8; DB 20;
Pred. No. 9.9e-05;
0; Mismatches 127;
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                                                                                                                                                                     Matches 177;
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1330
                                                                                                                                                                                                                                        Sequence 538 BP;
                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 175; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-261042/23.
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1997;
11-OCT-1996;
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  200
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                                                                                                                             794 gccgatagcggggggggggtacaccggatgcgacaggtggcggcggcggcggtgatacgcca 853
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Pred. No. 0.00023;
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                                                                                                                                                                            This is the 3' region of DNA coding for an antigenic portion of mycobacterium tuberculosis antigen xP22; 5' DNA is provided in AAV44436. XP22 DNA was isolated from a M. tuberculosis strain | genomic DNA expression library using sera from patients having sextrapplmonary tuberculosis. It bears no similarity to known extrapplmonary tuberculosis. It bears no similarity to known
                                                                                                                                                                                                                                                                                                   New isolated Mycobacterium tuberculosis polypeptides and to develop products for the detection of M. tuberculosis and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1151
                                         tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and
                                                                                                                                   sequences. The invention relates to methods and compositions diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble
                                                                                                                                                                                                                                                                           Claim 4; Page 186; 250pp; English.
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Reed SG, Skeiky YAW,
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                                                                                 1091 aatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgca 1150
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Search completed: October 4, 2001, 22:25:43 Job time: 5894 sec

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3 US-08-756-3068-9
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US-09-120-817-1
US-07-977-434-7
ALIGNMENTS
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; LENGTH: 1729 base pair
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (geno
US-09-120-817-1
                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REFIERENCE/DOCKET NUMBER: 1960
REFERENCE/DOCKET NUMBER: 1960
TELEPHONE: (716) 263-1304
TELEPAN: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Collmer, ALL...
APPLICANT: Charkowski, Amy
APPLICANT: Alfano, James R.
TITLE OF INVENTION: HYPERSENSITIVE
TITLE OF INVENTION: PSEUDOMONAS SY
TITLE OF SEOUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/120,817 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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Y: U.S.A.
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                                                                                                  1729 base pairs
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                     DNA (genomic)
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Score 1729; Pred. No. 0;

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GENERAL INFORMATION:
APPLICANT: GOId, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Tuerk, Craig
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION, Systematic Polypeptide E
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1990-08-02
NUMBER: O7/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER: OF SEQ ID NOS: 26
COMMENTANCE DEFORMS
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US-09-197-649-7
; Sequence 7, Application
; Patent No. 6194550
                                                                                                                   SOFTWARE: PatentIn
SEQ ID NO 7
FEATURE:
OTHER INI
OTHER INI
                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                 NO 7
TH: 390
INFORMATION:
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Description c
having a 120
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of Artificial Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-402-668-1'
                                                                                                                                                                                             APPLICANT: TSUMADORI, Masaki
TITLE OF INVENTION: Detergent Composition
FILE REFERENCE: 2173-0116P
CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
                                                                                                    SOFTWARE: PA
SEQ ID NO 1
LENGTH: 591
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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OTHER INFORMATION: Strain: KSM-P15
NAME/KEY: CDS
LOCATION: (1)..(591)
-09-402-668-1
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                     NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver.
                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 1998-04-09
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                                                                         TYPE: DNA
ORGANISM: Bacillus sp
                                                            FEATURE:
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KOBAYASHI, Tohru
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Pred. No. 1.3e-05;
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; ORGANISM: Bacillus licheniformis
US-09-198-956-3
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                                                                                Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 666
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Best Local Similarity 50.8%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09198956 Patent No. 6165769
                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 5377.200-US
CURRENT APPLICATION NUMBER: US/09/198,956
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-02
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER FILING DATE: 1997-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Andersen, Lene N.
APPLICANT: Schulein, Martin
APPLICANT: Lange, Niels Erik K.
APPLICANT: Bjornvad, Wads E.
APPLICANT: Schnorr, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Pectin Degrading Enzymes TITLE OF INVENTION: Licheniformis
                         1090 caatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgc 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1154 t---tcactgccgacaaatctatgggtaacgggggacaagggggaaaatcaggaagcccatg 1210
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cyaggtcgttcacaaaacgatcgtagtcgagaaaggccaaacgtatgacggaaaaggcaa 146
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                                                                                         Conservative
                                                                                                           3.2%;
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                                                                                         Score 55.8; DB 4;
Pred. No. 2.6e-05;
0; Mismatches 127;
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Pred. No. 1.6e-05;
0; Mismatches 199;
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US-08-232-463-14
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                                  Matches
                                                 Query Match
Best Local
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Patent No.
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1214 gagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcgatggc 1273
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                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
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                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                     LENGTH:
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                                    20;
                                                 Similarity
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5670367
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                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                   7218 base pairs
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                : (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                  Conservative
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                                                                                                                                                          linear
                                                                                                                                                                       single
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                                                 5.0%;
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                                 217;
                                                                                                                                                                                                                                   14:
                              Score 53.6; DB 1
Pred. No. 0.00024;
17; Mismatches 16
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                                                            DB 1;
                                 161;
                                                              Length 7218;
                                 Indels
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                              Gaps
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                                INFORMATION FOR SEQ ID NO:
                                                                          REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1454
                                                                                                                                                                                                                               PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect (Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/146,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
              SEQUENCE CHARACTERISTICS:
                                                                                                                                                     FILING DATE: October 29, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                             TELEFAX: (213)
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 90017
                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 611 West
CITY: Los Angeles
                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                        NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcaagcagtttgatgacatgagcatcgagctgaacggcatcgaagctaaccacggcaag 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08146930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   611 West Sixth Street
6530 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                       October 29, 1993
                                                               955-0440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFIC
                                                                                                                                                                                    No. 5958764 yet assigned (204/132)
                                                                                                                                                                                                                 including application described below: 07/876,286
                                                                                                                                                                                                                                                                                                               US/08/146,930
                                                                                                                      32,327
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Best Local Similarity 50.6
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: b11 ...
STREET: LOS Angeles
CITY: LOS Angeles
CTATE: California
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STRANDEDNESS: singl
TOPOLOGY: linear
MOLECULE TYPE: DNA (9
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APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3834 TCCTCTGGCGGCGGTGGCGGCGGTGGCTGCTACTCCAGCGGTGGTGGCGGCAGCAGCGGT 3893
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                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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FILING DATE:
APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
                                   TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                        October 29, 1993
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Pred. No. 0.0022;
0; Mismatches 117;
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                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            TOPOLOGY: 11near MOLECULE TYPE: DNA
                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03993
FILLING DATE: 19930428
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
ANTI-SENSE:
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
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ADDRESSEE: Fulbright & Jaworski
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CITY: Houston
                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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                                                                   STRANDEDNESS:
                                                                                                    LENGTH:
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                                                               H: 6530 base pairs
NUCLEIC ACID
DEDNESS: double
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Greenhalgh, David A.
Greenhalgh, David A.
VERTION: CONSTITUTIVE AND INDUCTBLE EPIDERMAL
VENTION: VECTOR SYSTEMS
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                              DNA (genomic)
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Pred. No. 0.0022;
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Length 6530;

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US-09-060-756-4
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                                                                                                                                             RESULT
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APPLICANT: Jacoom, Barry R.
APPLICANT: Jacobs Jr., William R.
TITLE OF INVENTION: iniB, iniA AND iniC GENE
TITLE OF INVENTION: OF USE
FILE REFERENCE: 96700/491
CURRENT APPLICATION NUMBER: US/09/177,349
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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                                                          Sequence 4, Application US/09060756 Patent No. 6183957 GENERAL INFORMATION:
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LENGTH: 5036
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Best Local
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Best Local Similarity
Matches 120; Conserv
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APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
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Local Similarity 51.2%;
les 111; Conservation
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Pred. No. 0.0022;
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US-08-118-200-1
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Best Local Similarity
Matches 100; Conserv
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                                                               COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SUTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED TITLE OF INVENTION: FRAGILE X SYNDROME NUMBER OF SEQUENCES: 13
                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                               STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                   E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
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LYNCH, Michael
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MULLEY, John C
MANDEL, Jean-Louis
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NAGARAJA, Ramaiah
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Robert I
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Pred. No. 0.0054;
0; Mismatches 8
                                                                        Version
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 20-MA

20-MAR-1991

US 07/672,232

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 05-DEC

NUMBER: US 07/802,650 05-DEC-1991

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Best Local :
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                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                  NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 020
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 836-6620
                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-JAN-1991 PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       448 CGGCGGCGGCGGCGGCGGCGGCCGGAGCCACC 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Alexandria
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mes 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
                            COUNTRY:
                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/966,517 FILING DATE: 23-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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               22313-1404
                                           Virginia
                                                                           P.O. Box 1404
                             United States
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MANDEL, Jean-Louis
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                                                                                                                                 DNA SEQUENCES RELATED TO ISOLATED FRAGILE X SYNDROME
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                                                                                         SWECKER & MATHIS
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Pred. No. 0.0056;
0; Mismatches 70;
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US-08-762-106-5
Sequence 5, Application US/08762106
Patent No. 5948677
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                   RESULT 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 04-JAN-1991
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Crane-Feury, Sharo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 23-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/802,650 FILING DATE: 05-DEC-1991 PRIOR APPLICATION DATA:
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                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                  STATE:
                                   COUNTRY: UZIP: 92037
                                                                                   CITY:
                                                                                              ADDRESSEE: Harris Brotman STREET: 202 Coast Blvd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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REFERENCE/DOCKET NUMBER:
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                                                                California
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Floppy disk
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                                                                                                                                                                Jonathan W.
READING FRAME INDEPENDENT EPITOPE
TAGGING
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56.0%;
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                                                                                                 Suite 111

 Mismatches

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Pred. No. 0.0056;
0; Mismatches 70; Indels
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US-08-762-106-6
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Best Local Similarity
Matches 101; Conserv
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APPLICANT: Jarvik, Jonathan W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1183
APPLICATION NUMBER: US/01
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1303 CCGCCGGCGGAGC 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Brotman, Harris F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                     CURRENT APPLICATION DATA:
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                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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CITY: La Jolla
STATE: California
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TYPE: nucleic acid
STRANDEDNESS: single
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.013;
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Best Local Similarity
Matches 101; Conserv
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Best Local Similarity
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 4-30582A
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                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                              LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
                                                                                                                 23789
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LENGTH: 1581 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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924 cacccactgcaacaggtggcggcaggcggtggcacaccccactgcaacaggcggtggcgagg 983
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                                                                 gcggtggcggcggtgatactccgaccgcaacaggcggtggcggcagcggtggcggcagcggca 923
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Db 23909 gggccggagcaggtggtgatcgcgggcgtggagcaagcggtgcaggcgatcgcgggggg 23968

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Search completed: October 4, 2001, 22:23:57 Job time: 6767 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

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57.4 56.8 55.2

52.6 51.5 50.6 50.6 50.6 49.8 49.4

genome

of the

Fisher, C.,

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GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis .
Tetraodon nigroviridis .
Tetraodon nigroviridis .
Tetraodon nigroviridis .
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

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library G fro
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AV175960
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AL104839 Drosophil
AW702254 TgESTZ274
BG417399 HVSMEK001
AL065629 Drosophil
AL109292 Drosophil
AL109292 Drosophil
AL533308 SD05070.5
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AW564035 LG1_281_D

BG35552 EM1_17_G1

AL254315 Tetraodon

AL106698 GH07623.5

BG444367 GA_Ea002

AW729119 GA_Ea002

AW729119 GA_Ea002
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AV199870 AV199870
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AI058502 UI-R-C1-k
AI114013 GH10644.5
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BG054210 OV2_2_G10
AL538536 AL538536
BE214873 HV_CEb000
AU172673 AU172673
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AL310686 Tetraodon
AW745859 WS1_37_C0
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AIS16351 S56 bp mRNA ES LD42191.5prime LD Drosophila melanogaster melanogaster cDNA clone LD42191 5prime, mR AIS16351 GI:4419451 EST. EST. fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 681)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis
Tetraodon nigroviridis DNA sequence
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Charaterization and repeat analysis
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Direct Submission
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llarity 43.1%;
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/db_xref="taxon:99883"
/clone="162H14"
/clone_11b="G"
/clone_11b="G"
/note="Genoscope sequence ID : CON-
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Pred. No. 0.00011;
7; Mismatches 202;
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    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiforme: Tetraodontidae; Tetraodon.

1 (bases 1 to 630)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                     Tetraodon nigroviridis
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Weissenbach,J.
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High quality sequence stop: 525.
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University of Callfornia Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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1 (Dases 1 to 556)
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,P., Lewis,S. and Rubin,G.M.
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/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="%XL1 Blue"
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/db_xref="taxon:7227"
/clone="LD42191"
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Pred. No. 0.00016;
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                               Dasilva, C., Fizames, C., Fisher, C
                                                                                         Percomorpha; Tetraodontiformes;
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                                                                                                                                                          AL053013.1
GSS.
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                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)
Direct Submission Submitted (02-JUN-1999)
                                      Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome. For more information, please thitp://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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/db_xref="taxon:99883"
/clone="110F12"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                            sequence.
AU161504
AU161504.1 GI:10931230
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- Web : www.genoscope.cns.fr)
                                                        Unpublished (2000)
                                                                      Sasaki,T. and Yamamoto,K. Rice cDNA from green shoot (2000)
                                                                                                     Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 327)
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/db_xref="taxon:7227"
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/clone="BACR19D16"
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AL109337
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Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                               Genoscope.
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 /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
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/db_xref="taxon:4530"
/clone="S16719"
                                                        Location/Qualifiers
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BP 191 91006 EVKY CELLON

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant are pavan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC BACN13L17 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthrópoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1034)
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/note="Green shoot (8 days old)"
54 c 180 g 58 t
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Pred. No. 0.0019;
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81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE024798 492 bp mRNA EST 894006B11.yl C. reinhardtii CC-1690, normalized, Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Elizabeth H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCMB Box 91000
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                     67
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/clone="BACN13117"
/note="end : T7"
a 256 c 236 g
            mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. FOLYA MRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5'y and XhoI (3') sites. pBluescript II SK-plasmids were excised from the lambda ZAP clones by superinfection with EXASSIST (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                             XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                                                                                                                                                                                                                                                                 /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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                                                                                       tggcggcggtgatacgccaagcgcaacaggcggtggcggtgatactccgaccgc
                                                                                                                                 VRGGRVCCAGGGASCACMAADCGGCCAKMACCSSSSASSSGSSCASTSSSASRGGMVSSC 742
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59; Conserv
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Direct Sub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   project grant. The DNA was prepared from embryos by and Genevieve Payan. It has been constructed in the
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176 c 160 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Pred. No. 0.0072;
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                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovegenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                       Characterization and repeat analysis of the compact freshwater pufferfish tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Crollius, H.R., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Boune Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J. Estimate of human gene number provided by genome using Tetraodon nigroviridis DNA sequence wat. Genet. 25 (2), 235-238 (2000)
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Tetraodon nigroviridis genome survey sequence T7
052H06 of library A from Tetraodon nigroviridis,
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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/clone_lib="A"
/note="Genoscope sequence
/note="Genoscope 342 g 234
                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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 Score 50; DB 221;
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cccactgcaacaggtggcggcagcggtgg
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                                                                                ggtggcggcggtgatactccgaccgcaacaggcggtggcggcagcggcggtggcggcaca
                                                                                                                      GGAGGCGGCGGATCCGGTGGTGGCGGACACAGCGGCCGCCATCATGGAGGCGGATGTGGC
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Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed t
below Phred quality 16. The t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: Unpublished (2000)
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/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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/db_xref="taxon:4558"
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Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                           AGCCAACTGGTGGAAAGCGGTCCTGATACCTACGCTCCAACTAGTGGCAACAGCAACA 402
                                                                                                                                                                   BF621686 824 bp mRNA EST 21-FEB-2001
HVSMEa0011N20f Hordeum vulgare seedling shoot EST library
HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa001
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Surveying Saccharomyces genomes to identify functional elements!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces kluyveri
Saccharomyces kluyveri
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Eukaryota; Fungi; Ascomycotaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ928169 541 bp DNA GSS 01-APR-2001
479.dif05d06.s1 Saccharomyces kluyveri Saccharomyces kluyveri
genomic clone 479.dif05d06.s1, DNA sequence.
                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University Medical School
Box 832, 4566 Scott Ave., St. Louis
Tel: 314 362 735
Fax: 314 362 7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comparative DNA sequence analysis Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces kluyveri.
                                                                          Hordeum vulgare
                                                                                                                       BF621686.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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135 c 168 g 158 t
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/clone_lib="Saccharomyces kluyveri"
/clone_lib="Saccharomyces kluyveri"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Saccharomyces kl/strain="NRRL Y-12651 (CBS/db_xref="taxon:4934"
                                                                                                                       GI:13083698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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AUTHORS
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                                                                                                                                                                                   Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditc
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditc
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 180)

Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki
Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A.,
Nishigaki, A., Motohashi, T., Zeng, Q., Thomashi, T., Sugimoto, A.,
Nishigaki, A., Motohashi, T., Zeng, Q., Thomashi, T., Sugimoto, A.,
Nishigaki, A., Motohashi, T., Zeng, Q., Thomashi, T., Sugimoto, A.,
Nishigaki, A., Motohashi, T., Zeng, Q., Thomashi, T., Sugimoto, A.,
Nishigaki, A., Motohashi, T., Zeng, Q., Thomashi, T., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV199870 180 bp mRNA EST 26-JUL-1999 AV199870 Yuji Kohara unpublished cDNA Caenorhabditis elegans clone yk552h11 3', mRNA sequence.
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Clemson University
100 Jordan Hall, Clemson, SC
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Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV199870
AV199870.1 GI:5583641
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On Dec 18, 2000 this
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                                                                                                                          Nomoto, H
                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                                                                          Miyata, A., Mitani, Y., Iida, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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HVcDNA0001 (Cold stress)"
/tissuc_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: Ecc
a 257 c 264 g 142 t
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/db_xref="taxon:4513"
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Best Local S
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AV175960
AV175960.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
Eukaryota; Metazoa; Nematodi; Rhabditidae; Peloderinae;
                                                                                                                                                                                                                         Yata 1111, Mishima, Shizuoka 411, Tel: 81-559-81-6854
                                                                                                                                                                                                                                                                               Contact: Yuji Kohara
Gene Library Lab
                                                                                                                                                                                                                                                                                                                                                                    Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M.,Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV175960 300 bp mRNA EST 21-JUL-1999 AV175960 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk499c4 3', mRNA sequence.
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Yata III1, Mishima, Shizuoka 4.
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                              National Institute of Genetics
                                                                                                                                                                                                                                                                                                                Expressed genes in C.elegans Unpublished (1999)
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Location/Qualifiers
                                                                                                                                                                 ykohara@lab.nig.ac.jp.
Location/Qualifiers
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="%referr"
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/sex="hermaphrodite, male"
/tissue="whole animal"
/dev_stage="varied"
96 c 20 g 32 t 7 o
                                                                                            /strain="N2"
/db_xref="taxon:6239"
                                                       /clone_lib="Yuji Kohara unpublished
                                                                         /clone="yk499c4"
                                                                                                                               organism="Caenorhabditis"
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derinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgcaacaggcggtggcggcagcggtggcggcacacccactgcaacaggtggcggcag 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI058502 343 bp mRNA
UI-R-C1-kv-d-01-0-UI.sl UI-R-C1 Rattus
UI-R-C1-kv-d-01-0-UI 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                     through Research Genetics This clone is also available thro
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1784479 The following repetitive elements were found in
cDNA sequence: 30-75, >(TGG)n#Simple_repeat 124-210, >(CGG
                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovery
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UJ-R-Cl-kv-d-01-0-UJ"
/clone_11b="UJ-R-Cl"
                                                                                                                                                                                                                                         Location/Qualifiers
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Search completed: October 4, 2001, 21:42:40 Job time: 4446 sec
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Best Local Similarity 55.6%;
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                      816 caccggatgcgacaggtggcggcggcggtgatacgccaagcgcaacaggcggtggcggcg 875
                                                                                                                                                        148 GTGGTCCGGGCAGCGCGGGGGGGGGGGGGGGGGGAC 196
                                                                                                                                                                                                                                                                                     44 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CI) was constructed as follows: PCR amplified cDNA inserts from UI-R-CO clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"
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Maximum DB seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Gapop 10.0 , Gapext 0.5
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//SIDS1/gcgdata/geneseq/geneseq/AA1990.DAT:*
/SIDS1/gcgdata/geneseq/geneseq/AA1990.DAT:*
/SIDS1/gcgdata/geneseq/geneseqD/AA1990.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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215	215	294.5	318	318	559	559	559	2200	2200	2200	Score
9.8	9.8	13.4	14.5	14.5	25.4	25.4	25.4	100.0	100.0	100.0	Query Match
752	730	221	197	197	447	447	447	424	424	424	% Query Match Length DB
21	21	20	19	19	21	21	20	21	21	20	:
AAG29581	AAG29582	AAY28446	AAW77412	AAW83014	AAY84855	AAY71094	AAW96260	AAY84859	AAY71098	AAW97851	ij
Arabidopsis thalia	Arabidopsis thalia	Bacillus lichenifo	Bacillus sp. pecti	Bacillus sp strain	A hypersensitive r	Erwinia amylovora	Hypersensitive res	A hypersensitive r	Pseudomonas syring	Hypersensitive res	Description

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AAY99354 AAB97551 AAB1205 AAB66103 AAG51723 AAW65201 AAG36620 AAG36619 AAG36619 AAG36618 AAY04999 AAW0926 AAW168207 AAW18575 AAW118573 AAW118573 AAW14574 AAW14574 AAW14574 AAW14574 AAW14574 AAW14574 AAW14574 AAW14574 AAW14574 AAW14574	AAP70709 AAW68205 AAY95559 AAY95556 AAG29727 AAB70182 AAW68203 AAW68203 AAW68213 AAW682116 AAW75865 AAW62457
Human PRO1411 (UNQ Human PRO1411. Ho Amino acid sequenc Protein of the inv Arabidopsis thalia M. catarrhalis str Arabidopsis thalia Mycobacterium spec M. catarrhalis str Human cyclin D1-hu	Plasmodium cynomol M. catarrhalis str Caenorhabditis ele Caenorhabditis ele Arabidopsis thalia Arabidopsis thalia Peptide dendrimer M. catarrhalis str Merozite surface a Hypersensitive res Pseudomonas solana Repeudomonas solana Hypersensitive re A hypersensitive r Pseudomonas solana Hypersensitive r Pseudomonas solana Hypersensitive r Mycobacterium tube

ALIGNMENTS

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	DA (CORR) CORNELL RES FOLIAD INC		XX PR 06-AUG-1997: 97US-0055107.	24-001-1996; 96WO-0513301.	7 7000		PD 18-FEB-1999.	XX	PN WO9907207-A1.			FT Domain 187424		Region 119186	FT domain"	/note= "	Domain	Key		OS. Pseudomonas syringae pv. tomato.	•	transgenic plant; disease resistance; insect	KW Hypersensitive response elicitor; dspE gene; HrpW;		DE Hypersensitive response elicitor HrpW.		DT 07-JUN-1999 (first entry)		AC AAW97851;		ID AAW97851 standard: Protein: 424 AA.	RESULT 1
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Matches 424;
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AAY71098;
                               AAY71098 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hypersensitive response eliciting (dspE) gene and protein useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
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                                                                                                                                                                                                 VRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQASTQ
                                                                                                                                                                                                                                                                    VHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTM
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                                                                                                                                                                                vrtnggkqfddmsielngieanhgkfalvksdsddlklatgniamtdvkhaydktqastq
                                                                                                                                                                                                                                                  vhaqnvgedlitvkgeggaavtnlniknssakgaddkvvqlnanthlkidnfkaddfgtm
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Pred. No. 7.5e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 25-26; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application of a hypersensitive response
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                   GHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDN
                                                                                                                                                                                                                               LGTPSADSGGGGTPDATGGGGGDTPSATGGGGGDTPTATGGGGSGGGTPTATGGGSGGT 180
HTEL
                                                                    VHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTM
                                                                                                                     ghgatftadksmgngdqgenqkpmfelaegatlknvnlgenevdgihvkaknaqevtidn
                                                                                                                                                                   ptatgggeggvtpqitpqlanpnrtsgtgsvsdtagsteqagkinvvkdtikvgagevfd
                                                                                                                                                                               PTATGGGEGGYTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFD
                                                                                                                                                                                                                 lgtpsadsggggtpdatgggggdtpsatgggggdtptatggggggtptatgggsggt
                                                                                                                                                                                                                                                               dstvqnpqdaskpndsqsniaklisalimsllqmltnsnkkqdtnqeqpdsqapfqnngg
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Pred. No. 7.5e-155;
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Matches 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants, especially vegetables and ornamental flowers -
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LGTPSADSGGGGTPDATGGGGGDTPSATGGGGGGDTPTATGGGGSGGTPTATGGGGSGGT
                            dstvqnpqdaskpndsqsnlaklisalimsllqmltnsnkkqdtnqeqpdsqapfqnngg
                                               DSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGG 120
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                                                                                                                                                              0
                                                                                                                                                          Score 2200; DB 21;
Pred. No. 7.5e-155;
Mismatches 0;
                                                                                                                                                            Indels
                                                                                                                                                                                          Length 424;
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RESULT
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                      The hypersensitive response eliciting protein (hrp) or polypeptide is produced as part of an active defense by plants against incompatible pathogen infections. The hypersensitive response is a rapid localised necrosis. The hrp protein and gene when used in nucleotide constructs are useful for providing disease resistance t plants, insect control to plants, and enhancing plant growth (enhancing fruit size and earlier colouration and maturation), by direct application of the protein to plants, or by producing transgenic plants or seeds using the hrp gene.
                                                                                                                                                                           New Erwinia amylovora hypersensitive response eliciting gene and protein - useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
                                                                                                                                                                                                                                           WPI; 1999-167126/14.
                                                                                                                                                   Claim 1; Page 50-51; 54pp;
                                                                                                                                                                                                                                                                    Beer SV,
                                                                                                                                                                                                                                                                                                                      06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypersensitive response elicitor protein; hypersensitive response; hrpW; pathogen; infection; crop protection; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORNELL RES
                                                                                                                                                                                                                                                                    Kim JF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; crop protection;
transgenic plant; colourat;
                                                                                                                                                                                                                                                                                             FOUND INC
                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  colouration; maturation
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Sequence

447

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RESULT AAYT1094
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XX AAYT
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The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a hypersensitive response elicitor protein from Erwinia amylovora. The protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypersensitive response elicitor; plant.
                                                                                                                         Disclosure; Page 10-12;
                                                                                                                                                                     Application of a hypersensitive response elicitor impart stress resistance -
                                                                                                                                                                                                                                                                                                                     Wei Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200028055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia amylovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia amylovora hypersensitive response elicitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71094;
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                                                                                                                                                                                                                                                                                                                                                                  (EDEN-)
                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998;
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                                                                                                                                                                                                                                                                   2000-376566/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPNRTSG------TGSVSDTAGS----TEQAGKINVVKDTIKVGAGEVFDGHGAT
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                                                                                                                         84pp;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat stable, protease sensitive and suppressed by inhibitors of metabolism. It is used to impart stress resistance to plants.
                                        N-PSDB; AAA14939.
                                                                    Wei Z,
                                                                                                             05-OCT-1998;
                                                                                                                                  05-OCT-1999;
                                                                                                                                                      13-APR-2000
                                                                                                                                                                         WO200020452-A2
                                                                                                                                                                                            Erwinia amylovora
                                                                                                                                                                                                                ornamental plant.
                                                                                                                                                                                                                         Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; c
                                                                                                                                                                                                                                                        A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                            08-AUG-2000
                                                                                                                                                                                                                                                                                                                   AAY84855 standard;
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                                                                                          (EDEN-) EDEN BIOSCIENCE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPNRTSG-----TGSVSDTAGS----TEQAGKINVVKDTIKVGAGEVFDGHGAT
                                                2000-303745/26.
                                                                                                                                                                                                                                                                                                                                                                   gqq-gnwdlnlshisaedgkfsfvksdseglnvntsdislgdvenhy
                                                                                                                                                                                                                                                                                                                                                                             GKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAY 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTADKSMGNGDQGENQKPMFELAEGATLKNYNLGENEVDGIHVKAKNAQEVTIDNVHAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sptkaaggstpvtdhpdpvgsagigagnsvaftsaganqtvlhdtitvkagqvfdgkgqt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGDTPTATGGGGSGGGTPTATGGG----SGGTPTATGGGEGGVTPQITPQL------A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TPSADS-----SATGGG-GDTP-----SATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qpidrqtieqmaqllaellksl---lspqsgnaatgaggndqttgvgnagglngrkgtag
                                                                     Fan
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                                                                                                              98US-0103050.
                                                                                                                                  99WO-US23181
                                                                    Niggemeyer
                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.4%; Score 36.1%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Mismatches
                                                                                                                                                                                                                                                                                                                    447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
l.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                            crop;
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Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plant: especially vegetables and ornamental flowers -

plants

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Best Local Similarity
Matches 147; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bear, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the proteins impart disease resistance to plants, enhance plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental
               WO9845393-A2
                                              Bacillus
                                                                             Bacillus sp. strain KSM-P15; pectic a protopectin; polygalacturonic acid; d cellulase; protease; bleaching agent.
                                                                                              Bacillus sp. protopectin;
                                                                                                                                              Bacillus sp strain KSM-P15 pectic acid lyase
                                                                                                                                                                               28-JAN-1999
                                                                                                                                                                                                               AAW83014;
                                                                                                                                                                                                                                                AAW83014 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 12-13; 100pp; English.
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                                                                                                                                                                                                                                                                                                                               gqq-gnwdlnlshisaedgkfsfvksdseglnvntsdislgdvenhy
                                                                                                                                                                                                                                                                                                                                                GKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAY 412
                                                                                                                                                                                                                                                                                                                                                                                                                               VGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMVRTNG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttpqsdsqnmlsemgnngldqaitpdgqgggqigdnpllkamlkliarmmdgqsdqfgqp 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPNDSQS--NIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLG-----
                                                                                                                                                                                                                                                                                                                                                                                               sptkaaggstpvtdhpdpvgsagigagnsvaftsaganqtvlhdtitvkagqvfdgkgqt 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPNRTSG-----TGSVSDTAGS----TEQAGKINVVKDTIKVGAGEVFDGHGAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtgnnsassgtsssggspfndlsggkapsgnspsgnyspvstfsppstptsptspldfps 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGDTPTATGGGGSGGGTPTATGGG---SGGTPTATGGGEGGVTPQITPQL-----A 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qpidrqtieqmaqllaellksl---lspqsgnaatgaggndqttgvgnagglngrkgtag 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TPSADS------SATGGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
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                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 559; DB 21;
Pred. No. 1.6e-33;
54; Mismatches 132;
                                                                                              pectic acid lyase;
c acid; detergent; c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132;
                                                                                              protopectinase;
cotton; surfacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
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RESULT
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Best Local S
Matches 74
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Shikata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a detergent composition which contains a protopectinase having an optimum pH 7 or higher against protopectin and polygalacturonic acid substrates. Inclusion of protopectinase gives a composition that provides better removal of muddy soll, particularly from socks. The present sequence represents pectic acid lyase from Bacillus sp. strain KSM-P15, which is used in an example from the present invention. Pectic acid lyase exhibits protopectinase
                                                                                                                                                                                                              AAW77412 standard; Protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detergent composition containing protopectinase active at alkaline pH - on protopectin and polygalacturonic acid, provides better removal of muddy soil
                                                                                       Bacillus sp. detergent; for
                                                                                                                                Bacillus
                                                                                                                                                         07-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-568339/48.
N-PSDB; AAV69879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1997;
09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-1998;
                                                              Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAOS ) KAO CORP
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                                                                                                                                                                                                                                                                                171 nt 172
                                                                                                                                                                                                                                                                                                          405 MT 406
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                                                                                                                                                                                                                                                                                                                                                                                                      285 GIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNAN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 VYKDTIKVGAGEVFDGHGATFTAD-KSMGNGDQGENQKPMFELAEGATLKNVNLGENEVD 284
                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                       gvhcyg----dctitnviwedvgedaltlkssg----tvnisggaaykaydkvfqinaa
                                                                                                                                                                                                                                                                                                                                                                                                                                         vvhetirvpaggtfdgkggtyvanpntlgdgsgaengkpifrleagaslknvvigapaad
                                                                                                                                                                                                                                                                                                                                  gtinirnfraddigklvrqnggtty-kvvmnvencnisrvkdailrtds---ststgriv
                                                                                                                                                                                                                                                                                                                                                            THLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                              ·ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 71-72; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ito S, Ka:
Suzumatsu
                                                                                      p. KSM-P15; pectic acid lyase; pectinic acid lyase; pectin; food-processing; fibre-processing agent; cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                              pectic acid lyase.
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0242736.
97JP-0091142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-JP01613.
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tsu A, Tsumadori M, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 318; DB 19; 40.7%; Pred. No. 3.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 197;
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5

14-OCT-1998

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RESULT
AAX/284
ID AAY2
XX AAY2
XX AAY2
XX Baci
DE Baci
XX Baci
XX Pect
KW Pect
KW Optil
KW recy
KW tran
XX ITAN
XX ITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a pectic acid lyase isolated from microorganism Bacillus sp. KSM-P15. The pectic acid lyase has high pectic acid lyase activity which degrades pectin in plant cell walls and fibre in vegetables, and so is useful as a component of detergents, a food-processing agent, or a fibre-processing agent. The pectic acid lyase has a higher optimum reaction pH (10.3-10.7) than known Bacillus pectic acid lyases (pH 8-9.5) and so has wider industrial applications. Details present pectic acid lyases, the new enzyme has a high enzyme
                                                                                                                                                                                              Pectate lyase I; EC 4.2.2.2; pectin degrading enzyme; ATCC 14580; catalytic active domain; cellulose binding domain; CBD; operably linked; optimum activity; pH; detergent composition; yarn; cellulosic fibre; recycled waste paper; pulp; retting process; animal feed; wine; juice;
                          Peptide
                                                                                                                      Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis Pectate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY28446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY28446 standard; Protein; 221 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Bacillus pectic acid lyase - useful as a food-processing agent and a fibre-processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-1997;
09-APR-1997;
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                                                                                                                                                                            transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity, and can be produced on a mass scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hatada Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAOS ) KAO CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 VVKDTIKVGAGEVFDGHGATFTAD-KSMGNGDQGENQKPMFELAEGATLKNVNLGENEVD
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gtinirnfraddigklvrqnggtty-kvvmnvencnisrvkdailrtds---ststgriv 170
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/label= Pro-sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    (CBD) that are operably linked to each other. It shows optimum activity at pH greater than 9 and temperature 55 degree centigrade. It can be use in detergent compositions, for cleaning hard surfaces, for machine treatment of fabrics, for improving the properties of cellulosic fibres yarn, woven or non-woven fabric, for the degradation of plant material e.g. recycled waste paper, mechanical paper-making pulps or fibres subjected to retting process, for preparing animal feed and for processing wine or juice. DNA encoding the enzyme can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is pectate lyase I, which is a pectin degrading enzyme derived from Bacillus licheniformis, ATCC 14580. The enzyme comprises a catalytic active domain and a cellulose binding domain
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                              nggtndgasgigsndgstgtnpg---agggtdsniegtennvggket-----np
                                                              HGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNV
                                                                                               snagg-----sksndganngasgiesnagstgtnfgaggtggigdtesdaggsktnsg
                                                                                                                                                                                                                                tnpgasa-----vgngeteknaggskpss----gsagtnpgasaggngeteknv
                                                                                                                                                                                                                                                                                                                             SPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGT---PDSTVQNPQDA--SKPNDSQSN 79
                                                                                                                                                               ggskpssgkagtnpganaggnggteknaggsksssgsartnpgasaggngetvsnigdte
                                                                                                                                                                                                                                                                                                                                                                 99;
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 215; DB 21; ilarity 24.0%; Pred. No. 8e-08; Conservative 46; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9903-0153758
9903-0154039
9903-0154039
9903-0155486
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9903-0155659
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99US-0160980

99US-0160989

99US-0161404

99US-0161406

99US-0161406

99US-0161350

99US-0161351

99US-0161351

99US-0161392

99US-0161993

99US-0161993

99US-0161993
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990S-0159584.
990S-0160741.
990S-0160767.
990S-0160767.
990S-016076814.
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99US-0151930.
99US-0152363.
                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                            Length 730;
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   361
                                                                301
                                 383
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09-MAR 1999
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26-APR 1999
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               9908-013047

9908-013049

9908-0130510

9908-013048

9908-0132407

9908-0132486

9908-0132486

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9908-013425

9908-013421

9908-013421

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99US-0126785.
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99US-0128234.
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AAG29581 standard; Protein; 752
                                                                                                                  Arabidopsis thaliana
                                                                                                                                                           termination sequence.
                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gasgig----
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2) 9.8%;
Similarity 24.0%;
99; Conservative
                                                              9908-0148341
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9908-0161361
                               ; Score 215; DB 21;
; Pred. No. 8.3e-08;
46; Mismatches 180;
                                                Length
                                Indels
                                88;
                               Gaps
                                  17;
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16-JUN 1999
17-JUN 1999
18-JUN 1999
18-JUN

9905-0139452.
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RESULT 12
AAP70709
ID AAP7077
XX AAP707
AC AAP707
XX DT 01-JAN
XX Immuno
XX Immuno
XX Immuno
XX Plasmo
XX 29-JAN
YX 24-JUN
YX 24-JUN
YX ARNO/
PR 12-JUL
XX WINT-
PA (ARNO/
YX WPI; 1
DR WP
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                         Query Match
Best Local (
                                                                                                                                                                                                                    The gene encoding the circumsporozoite protein of P. cynomolgi is used during the detection of the circumsporozoite protein of P. vivax. A DNA probe from this P. cynomolgi sequence, designated P236-7, is useful in the construction of an anti-malarial vaccine.
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                              Disclosure; fig. 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           New Plasmodium vivax circumsporozoite protein - and peptide(s) contg. its dominant epitope, useful in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN71065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnot DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP70709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP70709 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNY-) NEW YORK UNIV.
(ARNO/) ARNOT D E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogen; vaccine; malaria; immunodominant epitope; DNA probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GG-----GGDTPSATGGGGGGDTPTATGGGGSGGGG---TPTATGGGSGGTPTATGGGE
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                         Similarity
                                                                                                                                                                                             AAP70704-08
                                                                                                                                         402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cynomolgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cynomolgi sporozoite circumsporozoite protein
9.1%;
ilarity 32.4%;
Conservative 1
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                                                                                                                                                                                                AAN71064
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Pred. No. 4e-(
2; Mismatches
                                                   Score 201;
                         No. 4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nussenzweig
                                                   DB 8;
                                                   Length 402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 nd synthetic
anti-malarial
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Matches

60;

12;

85;

Indels

28;

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5

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RESULT 13
AAW68205
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                            This represents a UspAl antigen of Moraxella catarrhalis strain TTA24.

Nucleic acid sequences encoding the UspAl and A2 antigens of
M. catarrhalis isolates O355, O46E, TTA24 and TTA37 can be used in
G. M. catarrhalis isolates O355, O46E, TTA24 and TTA37 can be used in
G. genetic vaccination. An antigenic composition or vaccine containing
antigenic peptides from UspAl or UspA2 antigens are used to induce an
immune response in mammals against M. catarrhalis and can be used to
treat infections such as cittis media, sinusitis, lower respiratory
tract infections. They can also be used as immunity enhancers for other
bacterial, parasitic or viral antigens, to raise antibodies and as
immunoassay reagents for detecting specific antibodies. The antibodies
are useful for passive immunisation and as immunoassay reagents.
Detection of the epitopic core sequence, by immunoassay or by PCR, is
used to diagnose infection. The Usp antigens encoding nucleic acid
sequences are also used to produce recombinant proteins and for screening
for potential anti-M. catarrhalis agents, while their fragments are
                                                                                                                                                                                                                                                                                                                                                                      New peptide(s) containing the core epitope of Moraxella catarrhalis Usp proteins - useful in, e.g. vaccines to prevent or treat M. catarrhalis infection, and antibodies for passive immunisation
                                                                                                                                                                                                                                                                                                                                   Claim 30; Pages 152-155; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-377595/32.
N-PSDB; AAV41345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aebi C, Cope
Maciver I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis; UspAl; UspA2; antigen; genetic vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. catarrhalis strain TTA24 UspAl antigen
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               useful as diagnostic probes or primers or to isolate variant sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; otitis media; sinusitis; lower respiratory tract infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunity enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 yldki 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 EVDGI
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Sequence

941

8

Length

941; 113;

18;

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RESULT 1
AAY95559
ID AAY9
XX AAY9
AC AAY9
AC AAY9
AC Caen
XX Loca
KW Polly
XX WO2(
XX Synt
YX WO2(
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YX 06-(
YX 06-(
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location of vulva; LOV-1 gene; nematode; mating behaviour; polycystin; polycystic kidney disease; animal model; signal transduction; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
 Example 1; Page 131-139; 142pp; English
                                                     Isolated nucleic acid molecules from Caenorhabditis elegans useful for producing transgenic nematodes with altered mating behavior for identifying genes or regulatory factors involved in polycystic kidney
                                                                                                                              WPI; 2000-452537/39
                                                                                                                                                                Sternberg PW, Barr
                                                                                                                                                                                                                                        06-JAN-1999;
                                                                                                                                                                                                                                                                         06-JAN-2000; 2000WO-US00521
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                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                    (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 GNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQNVGEDLIT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 tiggghfntaegnystvgggftneaigknstvgggftneamgeystvaggannqakgnys 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGTPSADSGG------GGTP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMVRTNGGKQFDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGGS-----GGTPTATGG------GE-----GGVTPQITPQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---MSIELNG----IEANHGKFALVKSD 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     v-gagqisatstdavngsqlhalakavakn---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     algnkntiegtnsvälgsnntvktgkenvfilgsntntenaqsgsvllgnntagkaattv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LANPNRTSGTGSVSDTAGSTEQAGKINVV-----KDTIKVGAGEVFDGHGATFTADKSM 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tvgggngnkaignnstvvggsnnqakgehstiaggknnqatgngsfaagvenkadannav
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         avlgsllivgilgmattasagmatt...psaqvvktnnkkngthpfigggdynttkgnyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 8.2%; Score 179.5; DB 19; Length 1 Similarity 25.0%; Pred. No. 4.7e-05; 97; Conservative 39; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Query Match
Best Local Similarity
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                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a deletion allele, termed lov-1(sy582del), of the Caenorhabditis elegans LOV-1 protein (see AAY95556), generated by genomic deletion of the PKD/channel domain of the lov-1 gene by PCR. LOV-1 is an orthologue of the human polycystin-1 (PKD1) gene that is defective in human autosomal dominant polycystic kidney disease (PKD). The LOV-1 autosomal dominant polycystic kidney disease (PKD). The LOV-1 ransduction in sensory neurons. It is required for 2 male sensory behaviours, 'response' of males to hermaphrodites, and 'location' of the vulva. Nematodes such as C. elegans that express mutant or wild-type LOV-1 or PKD-2 (see AAY9557) can be used to study the functions of the proteins encoded by these genes, to screen for other genes involved in PKD, to identify mutations involved in the disease, and to screen for drugs that affect PKD. Behaviours controlled by the action of the genes or gene products are identified and used in the assays. Hence, an animal model is provided that permits study of the etiology of FKD and provides a tool to identify the genes involved in the disease pathway, to identify compounds that may be used to treat or alter the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY95556
                                                                                                                                       AAY95556 standard; Protein;
                                                                                                                                                                                                                                         1497 mat 1499
                                                                                                                                                                                                                                                                                                                    1437 iyltgdtrasykqldgdtvtadtmlaaaigiqgmfatngrtvqveqdkiddkrslvsgni 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101 sddaggktggt-gatggtgg-----tgsggsattlstgdavrsttsgsgsggsstgsgag 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 SADSGG--GGTPDATGGGGGGDTPSATGGGGGGDTPTATG------GGGSG 165
                                                                                                                                                                                                                                                                                404 AMT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 ----ATLKNVNLGE------NEVDGI-----HVKAKNAQEVTIDNVH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 VSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEG
                                                                                                                                                                                                                                                                                                                                                                                                 slnsvlssldlalkgstvytlgvsstkskdgtyavifgyviasgytlvsprctlsiygst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AQNVGEDLITVKGEGGAAVTNL-----NIKNSSAKGADD--KVVQLNANTH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rsslatvspisaaeqaiidaqkadvmnqlagimdgsasnnslntsssllnqisslpaadl 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gsdsngssgvstksssgsdt------sgssdssgangafsataqpstrttkt 1256
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                                                                                                                                                                                                                                                                                                                                                       VRTNGG-----KQFDD-------MSIELNGIEANHGKFALVKSDSDDLK--LATGNI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                          2870 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lessen its severity or ameliorate symptoms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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Pred. No. 0.00029;
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19;

Location of vulva; LOV-1 gene; nematode; mating behaviour; Caenorhabditis elegans LOV-1 (location of vulva) protein. 10-OCT-2000

(first entry)

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'location' of the vulva. Nematodes such as C. elegans that C. express mutant or wild-type LOV-1 or RKD-2 (see AAY95557) can be used to study the functions of the proteins encoded by these genes, to CC screen for other genes involved in PKD, to identify mutations CC involved in the disease, and to screen for drugs that affect PKD. CC Behaviours controlled by the action of the genes or gene products CC are identified and used in the assays. Hence, an animal model is provided that permits study of the etiology of PKD and provides a C col to identify the genes involved in the disease pathway, to C identify compounds that may be used to treat or alter the disease C progression, lessen its severity or ameliorate symptoms.
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Best Local S
Matches 96
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                                                                                                                                      1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101 sddaggktggt-gatggtgg-----tgsggsattlstgdavrsttsgsgsggsstgsgag 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 114-123; 142pp; English.
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signal transduction.
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les 96; Conserv
GGGTPTATGGGSGGTPTATGGGEGGGTPQITPQLANPNRTSGT------GS 210
                                                            ---AQNVGEDLITVKGEGGAAVTNL-----NIKNSSAKGADD--KVVQLNANTH----- 346
                                                                                                                                rsslatvspisaaeqaiidaqkadvmnqlagimdgsasnnslntsssllnqisslpaadl 1316
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                           404 AMT 406
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                                                                                                                     slnsvlssldlalkgstvytlgvsstkskdgtyavifgyviasgytlvsprctlsiygst 1436
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Result
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.
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US-08-460-746A-4
US-08-460-066-4
US-08-460-066-4
US-08-819-539-7
US-08-90-2070-7
US-08-919-539-7
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AT TOWNERS	US-08-276-852-34	US-08-808-599A-24	US-08-496-944-2	US-09-060-756-728	PCT-US91-09133-27	US-08-923-854-26	US-08-463-667A-4	US-08-463-587A-26	US-09-206-537-8	US-08-845-998-8	US-08-387-942C-5	US-08-808-599A-3	US-08-728-626-3	US-08-738-975-3	US-08-751-965-3	US-08-439-818A-3	US-08-317-522A-3	US-09-402-668-10
	Sequence 34, Appl	Sequence 24, Appl	Sequence 2, Appli	Sequence 728, App	Sequence 27, Appl	Sequence 26, Appl	Sequence 4, Appli	Sequence 26, Appl	-	Sequence 8, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 10, Appl					

; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-120-817-2 RESULT 1 US-09-120-817-2 Sequence 2, Apprix TELEFAX: (716) 263-160 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: APPLICANT: COllmer, Amy APPLICANT: Charkowski, Amy APPLICANT: Alfano, James R. TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR TITLE OF INVENTION: PSEUDOMONAS SYRINGAE AND ITS USE TITLE OF SEQUENCES: 8 REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19603/1741 TELECOMMUNICATION INFORMATION: TELEPHONE: (716) 263-1304 TELEPHONE: (716) 263-1304 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60 FILING DATE: 06-AUG-1997 ATTORNEY/AGENT INFORMATION: NAME: Goldman, Michael L. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Rclease #1.0, CURRENT APPLICATION DATA: STRANDEDNESS: FILING DATE: CLASSIFICATION: CITY: Rochester STATE: New York ZIP: 14603 COUNTRY: APPLICATION NUMBER: US/09/120,817 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square LENGTH: amino acid Application US/09120817 424 amino acids U.S.A. 6) 263-1304 263-1600 ID NO: 2: 60/055,107 Version #1.30

Query Match
Best Local Similarity
Matches 424; Conserv

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Score 2200; DB 4; Pred. No. 1.7e-172; Mismatches

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LENGTH: 197
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Applic Patent No. 6172030
                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: 9-24
PRIOR FILING DATE: 1997-09-08
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 1998-04-09
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR FILING DATE: 1997-04-09
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TSUMADORI, Masaki
TITLE OF INVENTION: Detergent Composition
FILE REFERENCE: 2173-0116P
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                      ORGANISM: Bacillus sp.
OTHER INFORMATION: Strain: KSM-P15
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226 VVKDTIKVGAGEVFDGHGATFTAD-KSMGNGDQGENQKPMFELAEGATLKNVNLGENEVD 284
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                             Local Similarity hes 74; Conserv
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SHIKATA, Shitsuw
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KOBAYASHI, To
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUZUMATSU, Atsushi
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                             14.5%; Score 318; DB 4
40.7%; Pred. No. 7e-19;
tive 33; Mismatches
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                                                        DB 4; Length 197;
                             61;
                             Indels 14;
                             Gaps
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RESULT 4
US-09-052-995-1
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Best Local Similarity
Watches 72; Conserve
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                                                       Sequence 1, Application US/09052995 Patent No. 6183956
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APPLICANT: Andersen,
APPLICANT: Schulein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 221
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CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER FILING DATE: 1997-12-02
GENERAL INFORMATION:
APPLICANT: Sivara
APPLICANT: Strulo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lange, Niels Erik K.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Schnorr, Kirk
TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
FILE REFERENCE: 5377.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-198-956-4
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                           189 STSSVTMTNTRYSKVGQKWIGVKHATER 216
                                                                                                                                                                                                               399 ATGNIAMTD-----VKHAYDK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                 219 EQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 MT 406
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                                                                                                                                                                                                                                                                                                                                   84 GAPAADGVHTYG----NASINNVVWEDVGEDALTVKSEG----SVTINGGSARLAADKI 134
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                                                                                                                                                                                                                                                                                                                                                                                                               EKALAAEVVHKTIVVEKGQTYDGKGKRLIAGPELGDGSQREDQKPIFKVEDGATLKNVVL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVHCYG----DCTITNVIWEDVGEDALTLKSSG-----TVNISGGAAYKAYDKVFQINAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIHVKAKNAQEVTIDNYHAQNYGEDLITYKGEGGAAVTNLNIKNSSAKGADDKYVQLNAN 344
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                                                                                                                                                                                                                                                                                             VQLNANTHLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKL
 Sivaraja, Mohanram
Strulovici, Berta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%; Score 294.5; DB 4 34.6%; Pred. No. 6.9e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 221;
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APPLICANT:

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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50...
36; Conservative
                                                                                                                                                                                                                                                                                                                                                 Sequence 40, Application US/09053003 Patent No. 6207391
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wu, Per
APPLICANT: MCKinn
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                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
            SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                           TITLE OF INVENTION: High-Throughput Screening Assays for TITLE OF INVENTION: Modulators of STAT4 and STAT6 Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 GGLGTPSADSGGGGTPDATGGGGGDTPSATGGGGGDTPTATGGGGSGGGTPTATGGGSG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 GTPTATGGGEGG 190
                                                                                                                        ZIP: 94111-3834
                                                                                                                                                                       CITY: San Francisco
APPLICATION NUMBER:
                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parent, Annette S. REGISTRATION NUMBER: 42,058 REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 31-MAI CLASSIFICATION: 43:
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(415) 576-0300
                                                                                                                                            USA
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McKinney, Judi
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                                PatentIn Release #1.0, Version #1.30
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 us/09/053,003
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Best Local :
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,987
FILING DATE: 03-SEP-1993
                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MATLASHEWSKI, Gregory APPLICANT: CHAREST, Hugues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
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                                                                                                         FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: M5G 1R7
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OTHER INFORMATION:
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nes 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canada
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(415) 576-0300
(415) 576-0300
(415) 576-0300
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/note= "Gly at positions 105-201 may
present or absent"
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/note= "Gly at positions 1-97 may be
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Pred. No. 1.1e-06;
0; Mismatches 36
                                                                                                                                                                                                                                                 Version #1.25
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US-08-460-746A-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                              FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHAREST, Hugues
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED LEISHMANIA
TITLE OF INVENTION: GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 KK 256
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                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 12-SEP-1994
                                                                                                                                                                               APPLICATION NUMBER: US/08/460,746A FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                           STREET: 6th Fi
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STRANDEDNESS: si
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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STEWART, Michael I.
STEWART, MICHAEL I.
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                  STEWART,
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                                                                                                                                                                                                                                                                                                                                                                                                  6th Floor, 330 University Avenue
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                                                  JMBER: US 08/115,987
03-SEP-1993
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                                                                                                                        US 08/302,463
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Pred. No. 1.7e-06;
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Best Local
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                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MATLASHEWSKI, Gregory
APPLICANT: CHAREST, Hugues
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED LEISHMANIA
TITLE OF INVENTION: GENES AND PROTEINS
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 03-SEP-1
CLASSIFICATION: 435
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                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                 APPLICATION NUMBER: US 08/302,463 FILING DATE: 12-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 PGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEG 148
                 NAME: STEWART, Michael REGISTRATION NUMBER: 2
                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sim & McBurney
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       RY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                               Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08460555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite 701, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                      03-SEP-1993
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NUMBER:
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31.9%;
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                                                                                                           US 08/115,987
                                                                                                                                                                                                                                                            US/08/460,555
                 24,973
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1038-485 MIS:vg
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Pred. No. 1.7e-06;
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TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155

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US-08-460-066-4
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Best Local s
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                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,463
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,987
FILING DATE: 03-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-484 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                          NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHAREST, Hugues
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED LEISHMANIA
TITLE OF INVENTION: GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 PDSQAPFQNNG-----GLGTPSAD----SGGGGT--PDATGGGGGGDTPSATGGGGGDT 155
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Suite
CITY: Toronto
                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/460,066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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31.9%;
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Query Match
Best Local Similarity
Watches 58; Conserva
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FRIGTH: 269 amino acids
                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,254
FILING DATE: 10-JUL-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
FILING DATE:
APPLICATION NUMBER: 08/475,775
FILING DATE:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFIERATION NUMBER: 14603/10050
TELECOMMUNICATION INFORMATION:
THE EMPLOYE: 7150, 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08891254 Patent No. 5776889
                                                                                TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
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                                    SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Induced Resistance In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wei, Zhong-Min APPLICANT: Beer, Steven V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: CITY: Rochester
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
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                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14603
                   amino acid
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                                                                                                                         (716) 263-1
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31.9%; Pred. No. 1.7e-06;
tive 14; Mismatches 68
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; MOLECULE TYPE: US-08-891-254-7

protein

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US-08-819-539-7
US-08-819-539-7
; Sequence 7, Application US/08819539
; Patent No. 5859324
; GENERAL INFORMATION:
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                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,539
FILING DATE: 17-MAR-1997
CLASSIFICATION BOO
PRIOR APPLICATION NUMBER: 08/475,775
APPLICATION NUMBER: 08/475,775
TELEPHONE: (716) 263-1304
                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 LGGGGAGAGGAGGADGGSGAGGAGGANGADGGNGVNGNQANG-------
                                       REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rochester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQILQQMLAAQNGGSQQST 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-MQLLEDLVKL-LKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIEQILAQ 172
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                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                               In Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
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Pred. No. 6.6e-06;
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US-09-030-270A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09030270A Patent No. 5977060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/039,226
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wei, Zhong-Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 L-MQLLEDLVKL-LKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIEQILAQ 172
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                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                             14603
                                                                                                                                                                                                                                                                                                                       Rochester
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                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                       E: Nixon, Hargrave, Devans & Doyle LLP P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                             U.S.A.
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INFORMATION
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                                                                                                                     US/09/030,270A
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US-08-984-207-7
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Best Local Similarity 20...
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08984207 Patent No. 6235974
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                          APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYDERSENSITIVE RESPONSE INDUCED
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TRI
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acid
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: GOLDMAN, Michael L.7
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1521
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                APPLICANT:
CURRENT APPLICATION DATA:
                                                                                                                     139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321
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                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Wei, Zhong-Min
Beer, Steven V.
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               PatentIn Release #1.0,
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23.2%; Pred. No. 6.6
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                                                                                                                                                                                                Devans & Doyle LLP
                 Version #1.30
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                                                                                                                                                                                                                                                         TREATMENT
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RESULT 14
PCT-US96-08819-7
; Sequence 7, Application PC/TUS9608819
; GENERAL INFORMATION:
TOTAL TRESEARCH Found:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
                                                                                                                                                                                       APPLICANT: Cornell TITLE OF INVENTION: TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             321 VQILQQMLAAQNGGSQQST 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 L-MQLLEDLVKL-LKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIEQILAQ 172
                                                                                                                                                                                                                                                                                                                                                                                                  294 QEVTIDNVHAQNVGEDLIT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                       279 GAGNASPASGANPGANQPGSADDQSSGQN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 LGGGGAGAGGAGGGVGGAGGADGGSGAGGANGADGGNGVNGNQANG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 -GGGGDTPSATGGGGGGTPTATGGGGSGGGGTPTATGGGGEGGVTPQITP 197
                                       COUNTRY: UZIP: 14603
                                                                              STATE:
                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 LIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGTPSADSGGGGTPDATG----- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AAQSAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQAPQSANKTGNVDDANNQDPMQA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                               CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 SALLFGSDT-----QKD--VNFGTPD-----STVQNPQDASKP-NDSQSNIAKLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNA 293
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                                                                          New York
                                                                                                               E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                                                                                                                                   Cornell Research Foundation, Inc.
IVENTION: HYPERSENSITIVE RESPONSE INDUCED
IVENTION: RESISTANCE IN PLANTS
                                                        U.S.A.
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263-17: 7:
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Pred. No. 6.6e-06;
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US-08-770-761A-8
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-08819-7
                                                                                                                                                                                    Sequence 8, Application US/08770761A Patent No. 5814503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.4%; Score 163.5; D
Best Local Similarity 23.2%; Pred. No. 6.6e-
Matches 88; Conservative 31; Mismatches
                                                                                                                                                                  GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 7:
                                    APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PRO
TITLE OF INVENTION: REGULATORY
NUMBER OF SEQUENCES: 8
                                                                                                                       APPLICANT:
APPLICANT:
                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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FILING DATE: 07-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 344 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-MQLLEDLVKL-LKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIEQILAQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQSAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQAPQSANKTGNVDDANNQDPMQA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALLFGSDT-----QKD--VNFGTPD----STVQNPQDASKP-NDSQSNIAKLISA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GGGGDTPSATGGGGGDTPTATGGGGSGGGTPTATGGGSGGTPTATGGGEGGVTPQITP 197
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                                                                                                                                            Kovacevic, Steven
Eli Lilly and Company
                                                            REGULATORY PROTEINS
                                                                                FUSION PROTEINS COMPRISING CELL CYCLE
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Best Local Similarity
Matches 99; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-DEC-199
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 317-376-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
459 ETIKDLMRQFLRGLD--FLHANCIVHRDLKPENILVTSGGTV
                                                                                 400 EVALLRRLEAFEHPNVVRLMDVCATSRTDREIKVTLVF-EHVDQDLRTYLDKAPPPGLPA 458
                                                                                                                                                                                                        215 AGSTEQAGKINVVKDTIKVGA-GEVF---DGHGATFTADKS--MGNGDQGENQKPMFELA 268
                                                                                                                                                                                                                                                                                              155 TPTATGGGGSGGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSGTGSVSDT 214
                                                                                                                                                                                                                                                                                                                                     270 AAEEEEEEEE---EEVDLACTPTDVRDVDIASMGGG-----SGGGSG------GGSGG- 314
                                                                                                                                                                                                                                                                                                                                                                               102 QDTNQEQPDSQAPFQNNGGLGTPS-----ADSGGGGTPDATGGGGGGDTPSATGGGGGD 154
                                                                                                                                                                                                                                                                                                                                                                                                                         211 AVQG-LNLRSPNNFLSYYRLTRFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNMDPK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 TPHDFIEHFLSKMPE----AEEN-KQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Lilly Corporate Center/Patent Division CITY: Indianapolis STATE: IN COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 TPLDF-SALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNF------GTPDS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                       VTNLNIKNSSAKGADDKVVQLNANTH--LKIDNFKADDFGTM
                                                                                                                                                                                                                                                      ---GSGGGSGGSGLSSKGGGGSG------GGGSGG-----
                                                                                                                      EGATLKNVNLGEN----EVDGIHVKAKNAQEVTIDNVHAQNVGEDLITVKGE----GGAA 320
                                                                                                                                                                -GGSMATSRYEPVAE-IGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGLPISTVR 399
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23;

Search completed: October Job time: 3858 sec

4, 2001, 22:26:02

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 45 summaries
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2: pir2:*
3: pir3:*
4: pir4:*
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hypothetical glyci
vsaA protein precu
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hypothetical glyci
glycine-rich prote
hypothetical glyci
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ALIGNMENTS

RESULT T18447

HrpW protein - Erwinia amylovora (;Species: Erwinia amylovora C;Species: Erwinia amylovora C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T18447 R;Gaudriault, S. submitted to the EMBL Data Library, May 1998 A;Reference number: Z18936 A;Reference number: Z18936 A;Reference number: T18447 The Control of the Co

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-447 <GAU
A;Cross-references: EMBL:Y13831; NID:e1293450; PID:e1293451; PIDN:CAA74158.1
A;Experimental source: strain CFBP1430; specific host Pommoideae
C;Genetics:

QY 366 GKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAY 412 	Qy 306 VGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMVRTNG	QY 246 FTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQN : : : : : : : : : : : : : : :	Qy 201 NPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGAT	Qy 152 GGDTPTATGGGGSGGGTPTATGGGSGGTPTATGGGEGGVTPQLTA 200	Qy 123 -TPSADSGGGGTPDATGGGG-GDTPSATGGG 151	Qy 72 KPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLG 122	Query Match 25.4%; Score 559; DB 2; Length 447; Best Local Similarity 36.1%; Pred. No. 1.7e-24; Matches 147; Conservative 54; Mismatches 132; Indels 74; Gaps
GNIAMTDVKHAY 412 : :: :: SDISLGDVENHY 435	LINANTHLKIDNEKADDEGTMVRTNG 365	NEVDGIHVKAKNAQEVTIDNVHAQN 305 : : : DGADGIHLYGDAKIDNLHVTN 329	AGKINVVKDTIKVGAGEVEDGHGAT 245 -	TGGGEGGVTPQITPQLA 200 : : : : : : : : : : : : : : : :	NPPSATGGG 151	NQEQPDSQAPFQNNGGLG 122	DB 2; Length 447; 7e-24; .es 132; Indels 74; Gaps 13;

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C;Species: Bacillus Subtilis
C;Catte: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Catte: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: A70045
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, F.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Reference number: A69580; MUID:98044033
A;Accession: A70045
A;Statius, Dreiffinary: nucleic acid sequence of the Gram-positive bacterium Bacillus subtilis.
A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
C;Superfamily: bromodomain homology
F;1723-1780/Domain: bromodomain homolog
                                                                                                                                                                                                                   A;Title: Drosophila CBP is a co-activator of cubitus A;Reference number: Z17785; MUID:97263578 A;Accession: T13828 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                CREB-binding protein homolog - fruit fly (Drosophila melanogaster) C;Specias: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000 C;Accession: T13828
                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-3190 < AKI>
A; Cross-references: EMBL: U88570;
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                                                                                                            A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                         R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Nature 386, 735-738, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15500.1; PID:e1186183
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-221 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 IHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANT 345
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bromodomain homology <BRO>
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                                                                                                                                       NID:g1916929; PID:g1916930;
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Pred. No. 7.3e-10;
2; Mismatches 71;
                                                                                                                                                                                                                                                                                                              interruptus in hedgehog signalling
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                                                                                                                                             PIDN: AAB53050.1
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
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Nature 408, 816-820, 2000
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A; Residues: 1-730 <STO>
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                                                                                                                                                                                                                       127 APPPGSTGAK--
180 TNPGASA---
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                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 24.0 
                                                                                                                                                                                                                                                                                                                  25 SPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGT---PDSTVQNPQDA--SKPNDSQSN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFTADKSMGNGDQGENQKPMFELAEGATLKNVN------LGENEVDGIHVKAKNA 293
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                                                                                                IAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGT-PSADSGGGGTPDATG 138
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     VGNGETEKNAGGSKPSS----
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; Pred. No. 5.8e-05;
46; Mismatches 180
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           -GSAGTNPGASAGGNGETEKNV 224
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Maiti, R.
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pectate lyase (EC 4.2.2.) C - fungus (Fusarium solani)
C;Species: Fusarium solani
C;Opate: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_cl
C;Accession: 568364
R;Guo, W.; Gonzalez-Candelas, L.; Kolattukudy, P.E.
Arch. Blochem. Biophys. 323, 352-360, 1995
A;Title: Cloning of a new pectate lyase gene pelC from Fusa
A;Reference number: 568364; MUID:96063610
A;Accession: 568364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <GUO>
A;Cross-references: EMBL:U13049
C;Genetics:
A;Gene: pelC
A;Introns: 52/1; 102/3
C;Keywords: carbon-oxygen lyase
probable myrosinase-binding protein - rape
N;Alternate names: jasmonate inducible protein
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1
C;Accession: T08080
R;Geshi, N.; Brandt, A.
Planta 204, 295-304, 1998
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                                                                                                                                                                                                                                                                                                                                      Y--DRGSGACKGQNEGGDKDAVFLLHEGATLKNVIIGKDQSEGVHCKG----HCTLEFVW
                                                                                                                                                                                                                                                                                                                                                       FTADKSMG---NGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVH 302
                                                                                                                                                                                                                                                                                                                                                                                                            GYTGGV-PKPTDHISN--
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                                                                                                                                                                                              SCGNCSKQCKRNVYIEGVTAKNGG------ELAGINANYGDTATLKNVCADAK 196
                                                                                                                                                                                                                                                                  FEDVCEDAISIKED -- KAGKESWIIGGGAYHASDKVVQHNGCGTVNIINFYVEDYGKLYR
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Pred. No. 5.
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                                                     21-May-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Two jasmonate-inducible myrosinase-binding proteins A;Reference number: 216340; MUID:98192006 A;Accession: T08080 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-680 <GES>
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                                                                                                                                   376 --LNGIEA---
                                                                                                                                                                                                                                                   443 YEEFELASDEYITIVEGYYDKILGSDGLTSLTFHTNKGTYGPYGLEGSTHFEFKEDGHKI 502
                                                                                                                                                                                                                                                                                                                                                                                                                                         236 GEVFDGHGATFTADKSMGN----GDQGENQKP-MFELAEGATLKNVNLGENEVDGIHVKAK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 KAGQPKQGALGGVQGSRGSTKEILINHPDEHLISVEGWYDSSNIIIGIQFKTNQKTSDYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 TGTGGTGTGGSGTGSGVEKLDAQGGTGGTAWDDGSDHDGVAKITVRTGGAGVQYVQFGYV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 -ANPNRTSGTGSVSDTAGSTEQA------GKINVV------KDTIKVG--A 235
                                                                                           QTYDGIGAVKFVYNKGSSEIIGDEHGKSTLLGFEEFELNYPSEYI--TEVHGTYDKISAS
                                                                                                                                                                       TGFHGRAGATISAIGVYLAPVGTIPLTPATQTKKLEAKGGDGGTTWDDGAFDGIRKVSVG
                                                                                                                                                                                                                                                                                                                               GGESGAVWDDGAHDNVKKVSVGQ------GTDGIAAVKFEYRNGSSVVIGAERGTPTLLG
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                                                                                                                                                                                                                                                                                                                                                                                                         GYDFDGSGTKFTL-QVQGKKIIGFHGFRQRPSQFNWERISVPVSTSTDPSTVPPKKLEAK 388
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                                                                                                                                                                                                             ---GTMVRT-------NGGKQFDDMSIE-----
                                                                                                                                 ---NHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQAS
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Pred. No. 0.00021;
3; Mismatches 139;
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                                                                                                                                                                                                                                                                                         --QLNANTH--LKIDNFKA
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H37RV)
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A; Molecule type: DNA
A; Residues: 1-1901 <COL>
A; Cross-references: GB: AL022022; GB: AL123456;
A; Cross-references: Strain H37Rv A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A; Title: Deciphering the biology of Mycobacterium A; Reference number: A70500; MUID:98295987 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares Nature 393, 537-544, 1998 hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 A; Gene: Rv3508 C; Superfamily: A; Experimental source: strain C; Genetics: A;Status: preliminary; nucleic acid sequence A; Accession: F70806 C; Accession: F70806 collagen alpha 1(IV) chain not shown; translation NID:g3261554; Whitehead, S.; Barrell, B.G. tuberculosis from the comple PIDN:CAA17745.1; Squares, S. not complete z D.; Holroyd, PID: g292 geno

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hypothetical protein R08B4.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T24045 R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-401 <GAL>
C; Comment: There are three distinct regions in the mature circumsporozoite protein,
                                                                                                                                                                                                                     Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obic membrane-anchoring sequence.

C;Comment: There are 17 tandem copies of the 11-residue repeat

C;Superfamily: circumsporozoite protein; thrombospondin type 1

C;Keywords: sporozoite; surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: major sporozoite surface antigen
C;Species: Plasmodium cynomolgi
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 48, 311-319, 1987
A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878
A;Accession: E26255
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R; Galinski, M.R.; Arnot, D.E.;
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Matches 86; Conservative
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                                                                                                                                                                                                                                                                    DGAAAAGGGGNDGAAAAGGGNGGAA - - - AGGGGNGGAAAGGGNGGAAAGGGNNA - - - - -
                                                                                                                                                                                                                          KDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGI
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3; Mismatches 87;
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Pred. No. 0.00028;
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hypothetical protein slr1403 - Synechocystis sp. (strain PCC 6803)
c;Species: Synechocystis sp.
A;Variety: PCC 6803
c;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
c;Accession: S77300
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; P.
c, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
S77300
밁
                                Ωy
                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-3016 <KAN>
A; Residues: 1-3016 <KAN>
A; Cross-references: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAA17634.1;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                         A; Reference number: S74322; MUID:97061201
A; Accession: S77300
A; Status: nucleic acid sequence not shown;
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A;Map position: X
A;Introns: 53/2; 113/1; 152/3; 204/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    맒
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z68008; FA;Experimental source: clone R08B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1226 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T24045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, A; Reference number: Z19834
                                                                                                                                                                                                                                                                                                                                         A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
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                                       22
                                                                            Local Similarity
les 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 QMLTNSNKKQDTNQEQPDSQ-APFQNNGGLGTPSADSGGGG----TPDATGGGGGGDTPSA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 QNTQQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDAS-KPNDSQSNIAKLISALIMSLL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 IGITPRP-----
                                                                                                                                                                                                                                                                                                                                       Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                     SGKSPQPNTFGEQNTQQAIDPSALLFGS------DTQKDVN-----FGTPDSTVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGGGDTPTATGGGSGGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HNTRNL----AKLMTRAVQK--RFGTTFESVVAEADFSWGTNKFNGRTCKIDS-----
  AGANASPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG----AGNGNGAGAGN----GNGAGAG---NGNGAGAGNGNGAGAGDASAAAAAAQAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QGYNALTYQSSSKPPPPSDFIDIPNDPTLGGPTGSSGGGGGGGGGGGGGGGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
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                                                                              Conservative
  -----IDMTGIAAGTIILNSPLPTLNNRNDITFVTLGAFGTPTIKFN 2458
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                                                                            8.8%; Score 194; DB 2;
20.9%; Pred. No. 0.0046;
tive 63; Mismatches 180
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26.9%;
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                                                                                180;
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                                                                                                                 Length 3016;
                                                                                Indels
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                                                                                204;
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da, м.; Yas
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99

NPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQA----

113

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A;Cross-references: FlyBase:FBgn0004656
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status pred:
F;1-1106/Product: female sterile homeotic protein, 110K #status pred:
F;59-116/Domain: bromodomain homology <BRO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         k; Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, 1 Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect A; Reference number: A43742; MUID:89276730
A;Accession: A43742
                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-2038 <HAY>
A;Cross-references: EMBL:M23221; NID:g157452; PIDN:AAA28540.1; PID:g157453
A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster) N;Alternate names: membrane protein fsh, 205K N;Contains: female sterile homeotic protein, 110K
                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:M23222
C;Genetics:
                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1106 <HA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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Conservative
                                                                                                   bromodomain homology
                   8.8%;
24.0%;
40;
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                   Score 193; DB 2;
Pred. No. 0.0033;
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Mismatches
                                                                                                     <BR02>
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133;
                                    Length 2038;
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Indels
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                                                                                                                                            <MA2>
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A;Experimental Source: liposarcoma R;Rabbitts, T.H.; Forster, A.; Larson, R.; Nathan, P. Nature Genet. 4, 175-180, 1993
A;Title: Fusion of the dominant negative transcription regulator CHOP with A;Reference number: S36157; MUID:93350637
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-binding protein FUS, nuclear - human N;Alternate names: RNA-binding protein TLS C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S33799; S36157 R;Crozat, A.; Aman, P.; Mandahl, N.; Ron, D.
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                                                                                                                                                                                                                                                A;Description: RNA binding; probable plays a role in transcriptional regulation C;Superfamily: RNA-binding protein EWS; ribonucleoprotein repeat homology C;Keywords: carcinogenesis; nucleus; RNA binding; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-63'S', 66-526 <RAB>
A; Cross-references: EMBL:X71428; NID:g393415; PIDN:CAA50559.1; PID:g4210363
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A;Map position: 16p11.2-16p11.2
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                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: liposarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:S62140; NID:g386156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S33798; MUID: 93288139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Fusion of CHOP to a novel RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Crozat, A.;
Nature 363, 6
                                                                                                                                                                                                                               ;286-361/Domain: ribonucleoprotein repeat homology
                                                                                                                                                 Query Match
Best Local
                                                                                                                            Matches
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  QKDVNFGTPDSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQP--
                                                                                 QQTTTPLDFSALSGKSPQPNT-----
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                                          QQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYG-STGGYGSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt VSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEG}
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96; Conser
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                                                                                                                                                                                                                                                                                                                                                       OMIM: 137070
                                                                                                                                             Score 191.5; DB 1
Pred. No. 0.00082;
                                                                                                                            Mismatches
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hypothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain H37 C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70807 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 R.; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Althors: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987
RESULT
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C;Superfamily: collagen alpha 1(IV) chain
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A;Residues: 1-1489 <COL>
A;Cross-references: GB:ALO22022; GB:AL123456; NID:g3261554; PIDN:CAA17751.1; PID:g292445
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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les 71; Conserv
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                                                                                                                                                                                                                                                                                       -GGSGGTPTATG----GGEGGVTPQITP-----QLANPNR--TSGTGSVSDTAGSTEQAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 189.5; DB 2;
Pred. No. 0.0036;
2; Mismatches 74;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: A70893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fus-like protein - human (fragment)
C;Specites: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: G02127
R;Itoh, K.; Kawase, M.
submitted to the EMBL Data Library, September 1995
A;Reference number: G09199
A;Accession: G02127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical glycine-rich protein Rv1067c - Mycobacterium tuberculosis (strain c;Species: Mycobacterium tuberculosis c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Nov-1999 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Nov-1999 C;Accession: A70893
A;Gene: Rv1067c
C;Superfamily: unassigned collagens
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A; Residues: 1-528 <ITO>
                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-667 <COL>
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                                                                                                                A; Cross-references:
                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                    ices: GB:AL021897; GB:AL123456; NID:g3256022;
source: strain H37Rv
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Result
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FUS_BOVIN
YP91_MYCTU
N145_YEAST
Y140_MYCTU
RICI_MOUSE
GRP1_PAWU
N145_YEAST
Y140_MYCTU
RICI_MOUSE
GRP1_PACTU
SWP1_ENCCU
FIF1_DROME
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drosophila
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mycobacteri

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119 GGLGTPSADSGGGGTPDATGGGGGGDTPSATGGGGGG---DTPTATG------GGGSGGG 167

Query Match
Best Local Similarity 29.3
Matches 86; Conservative

9.0%; 13;

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17745 ; i, 11. Re 30 901	entry is copyrig ss Institute of informatics Institution fit institution s statement is n s a license agre to license@isb-	EFROM N.A. 3-98295987; PubMed=9634230 T., Brosch R., Parkhill J S.V., Eiglmeier K., Gas S (K., Basham D., Brown D., R., Devlin K., Feltwell T A., Seger K., Krogh A., S., Seeger K., Skelton S., K., Whitehead S., Barrell hering the biology of Myco e genome sequence."; 393:537-544(1998). THE M FRAMILY: BELONGS TO THE M	STANDARD; 1. 39, Crea 1. 39, Last 1. 39, Last 1. 39, Last 3.15. uberculosis cutes; Acti ; Corynebac ;	700 421	1210 161 174 645 749 924 351 423 593
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SEQUENCE FROM N.A.
MEDLINE-89276730; PubMed-2567251;
Gavnes S.R., Mozer B.A., Bhatla-Dey N., Dawid
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                                                                                                                                                                              EMBL; M23221; AAA28540.1; -.
EMBL; M23222; AAA28541.1; ALT_TERM.
EMBL; M15762; AAA70424.1; -.
EMBL; M15763; AAA70423.1; -.
EMBL; M15764; AAA70422.1; -.
EMBL; M15764; AAA70422.1; -.
EMBL; M15764; AAA70422.1; -.
                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apparent membrane proteins.";
Dev. Biol. 134:246-257(1989).
-:- FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION
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InterPro; IPR001487; -.
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                                                                                                                                                                         "The circumsporozoite gene of the Plasmodium cynomolgi complex."; Cell 48:311-319(1987).
-!- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMTI
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Nussenzweig R.S., Enea V.;
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Best Local S
Matches 90
SEQUENCE FROM N.A. (SHUKI 1000)
SEQUENCE FROM N.A. (SHUKI 1000)
MEDLINE-93350637; PubMed-7503811;
Rabbitts T.H., Forster A., Larson R., Nathan P.;
Rabbitts T.H., Forster A., Larson R., Nathan P.;
"Fusion of the dominant negative transcription regulator CHOP with "Fusion of the dominant negative transcription regulator CHOP with "Fusion of the dominant negative transcription alignant liposarcoma."
                                                                                                                                                                                                                                                                                 FUS_HUMAN
P35637;
01-JUN-1994
01-JUN-1994
01-OCT-2000
                                                                                                                                      Crozat A., Aman P., "Fusion of CHOP to a liposarcoma.":
                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003067; -.
Pfam; PF00090; tsp_l;
PRINTS; PR01303; CRCMSPRZOITE.
Malaria; Sporozoite; Repeat; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 FUS OR TLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M15100; AAA29536.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    Homo sapiens (Human).
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                                                                                                            363:640-644(1993).
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                                                                                                                                                                                                                                                         (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
PROTEIN FUS (ONCOGENE FUS) (ONCOGENE TLS) (TRANSLOCATED PROTEIN) (POMP75) (75 KDA DNA-PAIRING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQNVGE
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98
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                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                    to a novel RNA-binding
                                                                                                                                                                                                            Chordata;
Primates;
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278
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Pred. No. 0.00
27; Mismatches
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17 X 11 AA TANDEM REPEATS
A-A-G-G-G-G-N.
; 57D666268238503E CRC64;
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EMBL; S62140; AAB27102.1; -.
EMBL; S62138; AAB27103.1; ALT_SEQ.
EMBL; S71427; CAA50558 1; ALT_SEQ.
EMBL; X71428; CAA50559.1; ALT_SEQ.
EMBL; X71428; CAA50559.1; ALT_SEQ.
EMBL; AF071213; AAC35285.1; -.
EMBL; AF071213; AAC35284.1; -.
PIR; S33799; S33799.
HSSP; P09651; 1HA1.
InterPro; IPR000504; -.
InterPro; IPR001876; -.
Pfam; PF00076; rrm; 1.
Pfam; PF000641; zf-RanBB; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANCER RES. 54:2865-2868(1994).

CANCER RES. 54:2865-2868(1994).

PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-STRANDED DNAS AND D-LOOP FORWATION IN SUPERHELICAL DOUBLE-STRANDED DNAS AND D-LOOP FORWATION IN SUPERHELICAL DOUBLE-STRANDED DNA, MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY.

POUNT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES.

SUBCELLULAR LOCATION: NUCLEAR.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE)

AND A SHORT ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99369251; PubMed-10442642;
Bertrand P., Akhmedov A.T., Delacote F.,
"Human POMp75 is identified as the pro-or
POMp75 and POMp100 DNA homologous pairing
to cell prolifieration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20036580; PubMed=10567410; Baechtold H., Kuroda M., Sok J., Ron D., Lopez B.S., "Human 75-kDa DNA-pairing protein is identical to the TLS/FUS and is able to promote D-loop formation."; J. Biol. Chem. 274:34337-34342(1999).
                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94243799; PubMed-8187069;
Ichikawa H., Shimizu K., Hayashi Y., Ohki M.;
"An RNA-binding protein gene, TLS/FUS, is fused to ERG in
myeloid leukemia with t(16:21) chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 18:4515-4521(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morohoshi F., Ootsuka Y., Arai I
Munakata N., Ohki M.;
"Genomic structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
MEDLINE-99013873; PubMed-9795213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 235-244; 307-312;
                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
SIMILARITY: CONTAINS 1 RANBP-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND CHOP.

DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML)
BY A CHROMOSOMAL TRANSLOCATION T(16;21)(P11;222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: UBIQUITOUS.

DISEASE: A FORM OF MALIGNANT MYXOID LIPOSARCOMA
BY A CHROMOSOMAL TRANSLOCATION T(12;16)(Q13;P11)
                                                                                                        151900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Durrbach
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Best Local S
Matches 96
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P35527; Q14665;
Q1-JUN-1994 (Rel. 29, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
KERATIN, TYPE I CYTOSKELETAL 9 (CYTOKERATIN 9
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CONFLICT
SEQUENCE
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ZN_FING
                                                                 TISSUE-FOOT SOLE TISSUE; TISSUE-FOOT SOLE TISSUE; PROM N.A., AND PARTIAL SEQUENCE.

TISSUE-FOOT SOLE TISSUE;

MEDILINE-94/131202; PubMed=7507869;

Langbein L., Heid H.W., Moll I., Franke W.W.;

"Molecular characterization of the body site-specific cytokeratin 9: cDNA cloning, amino acid sequence, and specificity of gene_expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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   MEDLINE=90267446;
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          Homo sapiens (Human)
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338
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   PubMed=2140676;
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TG -> S (IN SHORT ISOFORM).
T -> N (IN REF. 4).
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BREAKPOINT FOR TRANSLOCATION
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ARG/GLY-RICH.
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88C8E263B7905549 CRC64;
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RR Rosen E.M., Meromsky L., Romero R., Setter E., Goldberg I.;
RT "Human placenta contains an epithelial scatter protein.";
RL Blochem. Biophys. Res. Commun. 168:1082-1088(1990).
RN [3]
RN [4]
RN Wartants Eppk Lys-160; GLN-162 AND TRP-162.
RX MEDLINE-94214498; PubMed-7512862;
RX MEDLINE-94214498; PubMed-7512862;
RX MEDLINE-94214499; PubMed-7512862;
RX MEDLINE-95164981; PubMed-7512862;
RX MESCHLER M., Schroek E., Royer-Pokora B., Franke W.W., Sperling K.,
RA Greech. 6:174-179(1994).
RA L. Genet. 6:174-179(1994).
RA L. Genet. 6:174-179(1994).
RA MEDLINE-95164983; PubMed-7522199;
RX MEDLINE-9516498; PubMed-752
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EMBL; X75015; CAA52924.1; -.
EMBL; Z29074; CAA82315.1; -.
EMBL; S69510; AAC60619.1; -.
PIR; B35494; B35494.
                                                                                                                                                                                         PRINTS; PRO1248; TYPE1KERATIN PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                    MIM; 144200;
                                                                                                                                                                   Disease mutation.
                                                                                                                                                                                                                Pfam; PF00038;
                                                                                                                                                                                                                           InterPro; IPR001664; -.
InterPro; IPR002957; -.
                                                                                                                                                                              ntermediate filament;
                                                                                                                                                                                                                                                          P02876; 2WGC.
                                                          152
461
152
188
207
299
322
   162
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460
622
187
206
298
321
460
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N -> K (IN EPPK).

/FTId=VAR_003822.

R -> Q (IN EPPK).

/FTId=VAR_003823.

R -> W (IN EPPK).
                                                                                COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
                                                                       COIL
                                                                                                                                TAIL.
                                                          POLY-GLY
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/FTId=VAR_003824

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SEQUENCE
                              Submitted -!- FUNCTI
                                                                                                         SEQUENCE FROM N.A. MEDILINE-9309980; PubMed-1464327; MEDILINE-9309980; PubMed-1464327; Mehrba Wimmer C., Doye V., Grandi P., Nehrba "A new subclass of nucleoporins that nuclear pore protein NSP1."; EMBO J. 11:5051-5061(1992).
                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-93054906; PubMed-1385442;
Mente S.R., Rout M.P., Blobel G.;
"A new family of yeast nuclear pore
J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                    01-UI-1993 (Rel. 26, Created)
01-FBE 1996 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NUCLEOPORIN NUP116/NSP116 (NUCLEAR PORE PROTEIN NUP116/NSP116).
NUP116 OR XMR047C OR XM9532.12C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                         Q02630;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                    YEAST
N116_YEAST
                                                                                                                                                                                                                                                                                           Saccharomycetales;
NCBI_TaxID=4932;
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                                                        Odell C.,
                                                                   STRAIN-S288C / AB972;
                                                                                     SEQUENCE FROM N.A.
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Ill C., Bowman S., Barrell B.G., Rajandream M.A.;
mitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
midtion: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLOCATION
THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
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/FTId=VAR_003825.
T -> SR (IN CAA82315).
; 898C3825D4B5ED94 CRC64;
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-!- SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
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S28925; S28925.
A44402; A44402.
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SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX
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                                             ASTQH
                                                                                           LIASEEKNNGSQNNDMNFKSKSEEQ---ETILGKPKMDEKETANGGERMV-LSSKNDGED
                                                                                                                                      -----NGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQ
                                                                                                                                                                                    DKAQIKVDPKLSISIDKKNNQIAISNQQEENLDESILKASELLFNPDKRSFKNLINNRKM
                                                                                                                                                                                                                             NSSAKGADDKV-VQLN-ANTHLKIDN-----
                                                                                                                                                                                                                                                                          FSKATVTNTVSYPIQPSATKIKADERKKASLTNAY-KMIPKTLFTAK-----LKTNNSVM
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37 x 6 AA APPROXIMATE REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2; wilkinson-Sproat J.; wilkinson-Sproat J.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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                                                                                                                      SSGTGSDGVNSGKTTALNGDGTGSGTATTPGSHLGDGGSTSGS
                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                    MW.
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                     Score 177.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLY/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
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NEVDGI-----HVKAKNAQEVTIDNVH-----
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    4D9D423060F0CA85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2329 AA
                                                                                                                                                                                                                                                                                                       .063
                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                  110;
                                                                                                                                                                                                                                                                                                                       Length 2329;
                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                  165;
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for
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                          EMBL; M34398; AAA39444.1; -
EMBL; U09189; AAA82152.1; -
PIR; A35628, A35628.
HSSP; P10968; IWGC.
MGD; MGI:96816; LOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LORI_MOUSE
P18165;
01-NOV-1990
01-NOV-1990
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCA.
LOCA.
Mus musculus (Mouse).
Mus musculus (Mouse).
Theria; Rodentia;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=90275605; PubMed=2190691;

Mehrel T., Hohl D., Rothnagel J.A., Longley M.A., Bundman D.,

Cheng C., Lichti U., Bisher M.E., Steven A.C., Steinart P.M.,

Yuspa S.H., Roop D.R.;

"Identification of a major keratinocyte cell envelope protein,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                      J. Biol.
                                                                                                                                                                                                                                                                                "The proximal promoter of the mouse loriorin gene contains functional Ap-1 element and directs keratinocyte-specific bdifferentiation-specific expression";
J. Biol. Chem. 270:10792-10799(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 61:1103-1112(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LORICRIN
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Roop D.R.
                                                                                                                                                                                                                                                                                                                                                         DiSepio D., Jones A., Longley M.A., Bundman D., Rothnagel J.A.,
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95256248; PubMed=7738016;
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB,
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 MAT
                                                                                                                                                                                                                                                   Biol. Chem. 270:10792-10799(1995).
FUNCTION: MAJOR KERATINOCYTE CELL ENVELOPE PROTEIN.
SUBUNIT: MONOMERS ARE CROSSLINKED BY DISULFIDE AND N-(GAMMA-
                                                                                                                                                                                                                                     GLUTAMYL) LYSINE ISODIPEPTIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRTNGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEVAQSLLSNTLKIPGVGNMSSVDVLKTLQDNIATTNSELADEMAKVITKLANVNMTSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSLATVSPISAAEQAIIDAQKADVMNQLAGIMDGSASNNSLNTSSSLLNQISSLPAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AONVGEDLITVKGEGGAAVTNL----NIKNSSAKGADD--KVVQLNANTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYLTGDTRASYKQLDGDTVTADTMLAAAIGIQGMFATNGRTVQVEQDKIDDKRSLVSGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLNSVLSSLDLALKGSTVYTLGVSSTKSKDGTYAVIFGYVIASGYTLVSPRCTLSIYGST 587
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   481 AA;
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(Rel.
(Rel.
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35,
   37830
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Last annotation updat
   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MSIELNGIEANHGKFALVKSDSDDLK--LATGNI
   97349A786FF239FE CRC64;
                                                                                                                                                                                                                                                                                                               keratinocyte-specific but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                              ormatics and the EMBL outstat:
There are no restrictions on ong as its content is in no
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Query Match

7.8%;

Score 172.5;

DB 1;

Length 481;

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                                           Query Match
Best Local S
Matches 84
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FUS_MOUSE
P56959;
01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                      Wetal-binding,
Metal-binding.
TIN 168 2
278
364
                                                                                                                                                        DOMAIN
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Regulation of pigpen expression in mouse embryos."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF224264; AAF70602.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-STRANDED DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED DNA. MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY (BY SIMILARITY).

SUBUNIT: COMPONENT OF MICTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
SGKSPQPNTFGEQNT-----QQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDASKPND 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGGGSSCGGGGYSGGGGTSCGGGSSGGGGGGSSQQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSGGTPTATGGGEGGVTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDT----
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                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                   PS00030; RRM_RNP_1;
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                              DNA-binding;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GGGTPDATGGGGGDTPSATGGGGGGTPTATG
                                                                                                                                                          52673
                                                                  7.8%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%;
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                                                                                                                                                          W.
                                           45;
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                                                                  Pred.
                                                                  Score 172.5; DB Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                     FALSE_NEG.
                                                                                                                                                                             ARG/GLY-RICH.
C4-TYPE (POTENTIAL)
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                                                                                                                                                                                                                                           GLN/GLY/SER/TYR-RICH GLY-RICH.
                                                                                                                                                                                                                      RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                          E06F231BFEED78D6 CRC64;
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alliegro M.A.,
                                                                                                                                                                                                                                                                                                            protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as its content
                                                                                     DB 1;
                                              122;
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                                           Indels 103;
                                                                                     Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                              Zinc-finger;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gh a collaboration -
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                                           Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV0747 PRECURSOR.
RV0747 OR MTV041.21.
MYCObacterium teter
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053810;
                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                             "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                          Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Hamlin N., Holroyd Davies R., Deviin K., Feltwell T., Gentles S., Hamlin N., Holroyd Davies R., Deviin K., Feltwell T., Gentles S., Hamlin N., Holroyd
SEQUENCE
                                              Hypothetical protein; Repeat; SIGNAL 1 30
                                                                                 Pfam; PF00934; PE;
                                                                                                                               EMBL; AL021958; CAA17514.1;
                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=1773;
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                                                                                                                TubercuList; Rv0747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ozaki L.S., Svec P., Nussenzweig R.S., "Structure of the plasmodium knowlesi circumsporozoite protein.";
                                                                                                                        EMBL; K00822; AAA19699.1;
EMBL; K00772; AAA29556.1;
PIR; A03389; OZZQAK.
InterPro; IPR000884; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godson G.N., Ellis J., Svec P., Schlesinger D.H., Nussenzweig V.; "Identification and chemical synthesis of a tandemly repeated immunogenic region of Plasmodium knowlesi circumsporozoite protei
                                                                           Pfam; PF00090; tsp_1; 1
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                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic region of Plasmodium Nature 305:29-33(1983).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                          PROSITE;
                                                     PRINTS; PR01303; CRCMSPRZOITE
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                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T. WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                YQ34_MYCTU
YQ34_MYCTU
P71933;
01-NOV-1997
01-NOV-1997
30-MAY-2000
MEDLINE=98295987; PubMed=9634230; Gordon S.T., Brosch R., Parkhill J., Barnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C. E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C. E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall N.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Create 01-NOV-1997 (Rel. 35, Last s 30-MAY-2000 (Rel. 39, Last a HYPOTHETICAL PE-PGRS FAMILY RV2634C OR MTCY441.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
SEQUENCE
                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                 Actinomycetales;
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Pfam; pF00934; PE; 1.

Hypothetical protein; Transmembrane.
DOMAIN 27 53 ALA-RIC
TRANSMEM 332 352 POTENT:
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TubercuList; Rv1983;
                                                                                                                                                                                 NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                        SSAKGADDKVVQLNANTHLKIDNFKAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQNVGEDLITV----KGEGGAAVTNLNIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKDTIKVGAGEVFDGHGATFTADKSMG-------NGDQGENQKPMFELAEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIGSTLRAANAAAAASTTALAAAGADEVSAAVAALFARFGQE--YQAVSAQASAFHQQFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGWGANGGAGGLGDGVG----VDRGTGGAGGRGGLLYGGYGVSGPGGDGRTVPLEI----
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558 AA;
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ilarity 22.4%;
Conservative '
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53738
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Last annotation
FAMILY PROTEIN R
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POTENTIAL.
POTENTIAL.
17ECBE43778E021E (
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3; Mismatches
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Pred. No. 0.
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RV2634C.
                                                                                                                                                                                                Mycobacteriaceae;
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Best Local
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                                                                                                                                                                               Drosophila
Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                      MAM_DROME
P21519;
01-MAY-1991
01-MAY-1991
01-MAR-1992
unusually rich in amino acid homopol
Genes Dev. 4:1688-1700(1990).
-i- FUNCTION: MAY HAVE A REGULATORY
WITH THE N GENE PRODUCT.
                                                                                 MEDLINE=91065516; PubMed=1701150; Smoller D., Friedel C., Schmid A.
                                                                                                                                                                                                                             MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                       "The Drosophila neurogenic locus unusually rich in amino acid homo
                                                                      Yedvobnick B
                                                                                                              STRAIN=CANTON-S;
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                           NEUROGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence.";
Nature 393:537-544(1998).
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 778 AA; 63131 MW;
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HSSP; P04002; IATF.
TubercuList; Rv2634c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute There are no restrictions on its content is in no way use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                    AGGKGGQGHNTGVGDAFGGD
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                                                                                                                                                                                                                                                                                                                                                                                                              EGGAAVTNLNIKNSSAKGAD
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76; Conservative
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                                                                                                                                                                   mclanogaster (Fruit fly).
Mctazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Metazoa; Arthropoda; Tracheata; Brachycera; Musc
Neoptera; Endopteryyota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                      (Rel. 18, Created)
(Rel. 18, Last sequence up
(Rel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                          GAG-----GIGETDG
                                                                                                                                                                                                                                                                                                               STANDARD;
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Pred. No. 0.048;
                                          homopolymers
                                                                                 Α.,
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opolymers.";
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                ASSOCIATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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PIR; A36391; A36391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER NUCLEAR PROTEINS OF DROSOPHILA, TO CERTAIN YEAST AND MAMMALIAN REGULATORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: DURING EARLY NEUROGENESIS MAM PRODUCTS ARE UBIQUITOUSLY LOCATED. DURING LATER STAGES THEY ACCUMULATE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR.
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                                                              DGIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGG 318
                                                                                                                                                                                            DGHGATFTADKSMGNGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGGGGSG-----PTATGGGSGGTPTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVTVKALTN-----TSVKSEPGVG-----GGGG-----GGGGGNSGNNNNNNGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSNTGNNTN-NNGNSTNNN----GGSNNNGSENLTKFSVEIVQQLEFTTSPANSQPQQIST 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSDTQKDVNFGTPDSTVQNPQDASKPNDSQSNIAKLISALIMSL------LQMLT 96
   DGIKVEPPNAQDLI--
                                                                                                                                                                                                                                                        AGGLGGMGMPPNMMSAQQKSALGNLANLVECKREPDHDFPDLGSLD-----KDGGGGQF
                                                                                                                                                                                                                                                                                                                       EGGVTPQ-ITPQLANPNRTSGTGSVSDTAGSTEQ-----AGKINVVKDTIKVGAGEVF 239
                                                                                                                                                                                                                                                                                                                                                                                   ---GGGGNGNNNNNNGGDHHQQQQQHQHQQQQQQQQGGGLGGLGNNGRGGGPGGMATGPGGV
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                                                                                                                             PGFPDLLGDDNSENNDTFKDLINNLQDFNPSFLDGFDEKPLLDI--
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ASN-RICH.
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W; B944D86EF359D605 CRC64;
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAG22 ANTIGEN PRECURSOR. WAG22 OR RV1759C OR MTCY28.25C.
                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                           Antigen; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY.
                                                                                                                                                            IAKLISALIMSLLOMLTNSNKKODTNOEQPDSQAPFONNGGLGTPSA--DSGGGGTPDAT 137
FLIGSGGTGGVGGAATTTGGVGGAGG----NAGLLIGAAGLGGCGGGAFTAGVTTG
                                \tt QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMG
                                                                GGNGGAGAAGTNGSAG-----GAGGAGGILFGTGGAGGAGGVGTAGAGGAGGAGG--SA
                                                                                             GGGGGDTPSATGGGGGGTPTATGGGSGGGTPTATGGGEGGVTPQITP 197
                                                                                                                               LQQDILSFINEPTEALTG
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914 AA;
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Pred. No. 0.06;
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                p93658 brassica na
Q00845 nectria hae
Q21835 caenorhabdi
P73590 synechocyst
Q9w313 drosophila
                                                                Q9w321 drosophila
Q00843 nectria hae
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176	176	176.5	177	177	177.5	177.5	178	178.5	178.5	179.5	179.5	180.5	181.5	182.5	183	184.5	185	185	185.5	186.5	186.5	187.5	188	188.5	189
8.0	8.0	8.0	8.0	8.0	8.1	8.1	8.1	8.1	8.1	8.2	8.2	8.2	8.2	&	& 3	8.4	8.4	8.4	8.4	8.5	8.5	8.5	8.5	8.6	8.6
618	447	1963	944	912	491	388	770	741	242	941	694	348	1381	1538	731	697	347	207	1079	869	240	813	667	705	528
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006801 mycobacteri	Q9sia8 arabidopsis	Q9xcq3 salmonella	Q9vk59 drosophila	Q9xd52 moraxella c	O06818 mycobacteri	Q94675 plasmodium	O85783 myxococcus	O06808 mycobacteri	Q04701 fusarium so	Q9xd54 moraxella.c	O53212 mycobacteri	093397 cyprinus ca	O53552 mycobacteri		O50415 mycobacteri	_	Q9gzc7 trypanosoma	Q43522 lycopersico	O53557 mycobacteri	Q9j3u0 ectocarpus	O93877 fusarium ox	Q50279 mycoplasma	O53415 mycobacteri	004310 arabidopsis	Q13344 homo sapien

ALIGNMENTS

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RESULT
087264
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087264;
01-NOV-1998
01-NOV-1998
01-CCT-2000
MEDLINE-20243785; PubMed-10781092;
Alfano J.R., Charkowski A.O., Deng W.L., Badel J.L.,
Petnicki-Cowleja T., van Dijk K., Collmer A.;
"The Pseudomonas syringae Hrp pathogenicity island has a tripartite mosaic structure composed of a cluster of type III secretion genes bounded by exchangeable effector and conserved effector loci that contribute to parasitic fitness and pathogenicity in plants.";
Proc. Natl. Acad. Sci. U.S.A. 97:4856-4861(2000).
EMBL; AF305221; AAC62526.1; ...
EMBL; AF302206; AAF71503.1; -..
EMBL; AF322006; AAF71503.1; -..
EMBL; AF32006; AAF71503.1; -..
                                                                                                                                                                                                                                                                                                                                                                      "The Pseudomonas syringae pv. tomato HrpW protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate.";
J. Bacteriol. 180:5211-5217(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98422476; PubMed=9748456; Charkowski A.O., Alfano J.R., Preston G.,
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                                                                                                                                                                                                                                                                                                                  STRAIN-DC3000;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 424; Conservative 0

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Score 2200; DB 2; Pred. No. 1.5e-128; ; Mismatches 0;

Length Indels

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Best Local Similarity
Matches 312; Conserv
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J. Bacteriol. 180:5211-5217(1998).
EMBL; AF037983; AAC62530.1;
SEQUENCE 441 AA; 44714 MW; 7B3B3146E51897BB CRC64;
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087327;
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Bacteria; Proteobacteria;
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01-NOV-1998 (TIEMBLIEL 08, La
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HRP TYPE III SECRETED PROTEIN.
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QPDNTVQNPTDSSAATDPQSNVVKLLSALVTSLLQMLMNLNKKQDTGQDSNEWQDPFQNE
                       TPDSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNN 118
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Alfano J.R., Pre
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Best Local Similarity 36.3
Matches 147; Conservative
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Q9LAW2;
01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                 Kim J.F., Laby R.J., Beer S.V.;

"Comparison of the hrpN-flanking regions of two Erwinia

strains with different host specificity.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF083620; AAF63402.1; -.

SEQUENCE 447 AA; 45340 MW; OBBAEA3871EDC2F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bactería;
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FTAGSELGDGGQSENQKPLFILEDGASLKNVTMGDDGADGIHLYG----DAKIDNLHVTN
                       FTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQN
                                               SPTKAAGGSTPVTDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDTITVKASQVFDGKGQT
                                                                                                 GTGNSSASSGTSSSGGSPFNDLSGGKAPSGNSPSGSYSPVSTFSPPSTPTSPTSPLDFPS
                                                                                                               TTPQSDSQNMLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARMMDGQSDQFGQP
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36.1%;
                                                                        -TGSVSDTAGS----TEQAGKINVVKDTIKVGAGEVFDGHGAT
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                  Score 563; DB 2;
Pred. No. 1.9e-27;
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VGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMVRTNG

VGEDAITVKPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFVRTNG

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Matches 147
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054508;
01-JUN-1998
                                                                                                             homologous to pectate lyases of a distinct class.";
J. Bacteriol. 180:5203-5210(1998).
EMBL; V13831; CAR74158 1; -.
EMBL; U97504; AACNARACA.
                                                                                                                                                                                                                                    STRAIN=EA321, ATCC 49947;
Kim J.F., Zumoff C.H., Beer S.V.;
"HrpW, a new harpin of Erwinia ampectate lyases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DspA, an essential pathogenicity factor of Erwinia amyl homology with AvrE of Pseudomonas syringae, is secreted secretion pathway in a DspB-dependent way."; mol. Microbiol. 26:1057-1069(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRPW
                                                                                                    EMBL; U97504; AAC04849.1; EMBL; U94513; AAC62314.1;
                                                                                                                                                                              STRAIN=EA321, ATCC 49947;
MEDLINE=98422475; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia amylovora.
Bacteria; Proteobacteria;
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01-NOV-1998
                                                                                                                                                                       Kim J.F
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     Bogdanove A.J., Kim J.F., Wei Z., Kolchinsky P., Conlin A.K., Collmer A., Beer S.V.; Conlin A.K., Collmer A., Beer S.V.; "Homology and functional similarity of an hrp-lin locus, dspEF, of Erwinia amylovora and the avirul Pseudomonas syringae pathovar tomato."; Proc. Natl. Acad. Sci. U.S.A. 95:1325-1330(1998).
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-138 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaudriault S
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CFBP1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 138-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98086111; PubMed=9426142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CFBP1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=552;
                                                                                                                                                                                                                            hytopathology 87:0-0(1997)
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KPNDSQS--NIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLG---
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ilarity 36.1%;
Conservative 5
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                                Score 559; DB
Pred. No. 3.4e
54; Mismatches
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                                3.4e-27;
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SEQUENCE
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Bacteria; Firmicutes; Bacteria; Staphylococcus
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01-MAY-2000
                                                                                                                                                                                                                                                                               EMBL; AB011839;
                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                         alkaline
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                                                               345 THLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIA 404
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198
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                                              GTINIRNFRADDIGKLVRQNGGTTY-KVVMNVENCNISRVKDAILRTDS---STSTGRIV
                                                                                                                                              VVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQKPIFRLEAGASLKNVVIGAPAAD
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                                                                                             GVHCYG----DCTITNVIWEDVGEDALTLKSSG-----TVNISGGAAYKAYDKVFQINAA
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                                                                                                                                                                                                                                                                                   acid sequence and possible Catalytic residues ne pectate lyase from alkaliphilic Bacillus."; ted (MAR-1998) to the EMBL/GenBart/MAR-1998).
199
                        406
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Pred. No. 1.1e
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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
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034310;
01-JAN-1998
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01-NOV-1998
   MEDLINE-98044033; PubMed-9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVPA.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soriano M., Blanco A., Diaz
Submitted (APR-1999) to the
EMBL; AJ37980; CAB40884.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PECTATE LYASE
PELA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus/Staphylococcus NCBI_TaxID=1423;
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SIGNAL
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                                                                                                                                                                                                                            STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                      Karamata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLVASIFGVMPAAAAPTVVNSTIVVPKGTTYDGQGKTFVANPSTLGDGSQAENQKPVFRL
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23233 MW;
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EMBL/GenBank/DDBJ
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1.7e-12;
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RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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O9EX16;

O1-MAR-2001 (TrembLrel. 16

O1-MAR-2001 (TrembLrel. 16

O1-MAR-2001 (TrembLrel. 1
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                          SEQUENCE FROM STRAIN=A3(2);
                                                                                                                                                               Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                          NCBI_TaxID=1902;
                                                                                                                                          Actinomycetales;
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D.C.,
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     Harris
                                                                                                                                          Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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Pred. No. 4.9e
32; Mismatches
                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                             Streptomycetaceae;
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                                                                                                                                             Streptomyces
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MEDLING-97263578; PubMed-9109493;

Akimaru H., Chen Y., Dai P., Hou D.X., Nonaka M.,

Armstrong S., Goodman R.H., Ishii S.;

"Drosophila CBP is a co-activator of cubitus inte signalling.";

Nature 386:735-738(1997).

EMBL; U88570; AAB53050.1; -.

HSSP; P03622; 2IFO.
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Best Local
                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CREB-BINDING PROTEIN HOMOLOG.
NEJ OR CG15319.
                                                                                                                                                                                                                                                                                001368
001368;
01-JUL-1997
01-JUL-1997
01-MAR-2001
                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL445503; CAC13062.1;
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Cerdeno A.M., Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-A3(2);
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                      bromodomain;
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 239; DB 2;
Pred. No. 1.1e-07;
5; Mismatches 74
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Best Local Similarity
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O9ZU23;
01-MAY-1999 (TREMBLRel. 1
01-MAY-1999 (TREMBLREL. 1
01-MAY-2000 (TREMBLREL. 1
                                                                                                            Li J., Kremenetskaia I., Luros J., Gonzalez A., Altafi H Buehler E., Conway A.B., Conn L., Dunn P., Hansen N., Hu Kim C., Palm C.J., Rowley Conn L., Shinn P., Walker M., Davis Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F5F19 sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006216; AAD12691.1; -.
HSSP; P18670; IJAC.
InterPro; IPR001064; -.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Vysotskaia V.S., S. Li J., Kremenetska
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PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS00633; BROMODOMAIN_1;
PROSITE; PS50014; BROMODOMAIN_2;
SMART; SM00291; ZnF_Zz; 1.
SEQUENCE 3190 AA; 331879 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
   SEQUENCE
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                                                      InterPro; IPR001229; -. Pfam; PF01419; Jacalin;
                              PROSITE; PS00225;
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   ΑĄ;
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CRYSTALLIN_BETAGAMMA; UNKNOWN_1.; 73939 MW; E4323AF993B1D95E CRC64;
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Pred. No. 5.2e
37; Mismatches
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Last sequence update)
Last annotation update)
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J., Gonzalez A., Altafi H., Araujo
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Query Match

Local

Similarity

9.8%;

Score 215; DB 10; Pred. No. 1.1e-05;

Length 730;

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RESULT 11

Q9W321

ID Q9W321

AC Q9W321

DT 01-MAX

DT 01-MAX

DT 01-MAX

DT 01-MAX

DT 01-MAX

DT 01-MAX

CC 251531

GN NEJ OPR

CC 251531

GN NEJ OPR

CC Pteryg

OC Pteryg

OC Pteryg

OC PTER

RA SEQUEN

RC STRAN

RC STRAN

RA Adams

RA Adams

RA Abril

RA Abril

RA Ballew

RA Berson

RA Berson

RA Berson

RA Borkov

RA Berson

RA Burtis

RA Cherry

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RA Harriss

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RA Liasko

RA Kimmell

RA Lasko
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RX MEDLINE-2019(606); PubMed-10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Rewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Ballew R.M., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bodshakov S.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bodshakov S.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Bavies P.,
RA Borkova D., Botchan M.R., Bouck J., Bavies P.,
RA Borkova D., Botan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Duzbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Duzbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N., Gulfara C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Q9W321;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGGTNDGASGIGSNDGSTGTNPG---AGGGTDSNIEGTENNVGGKET-----NP
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13,
16,
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Last annotation updat
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RESULT Q00843 ID Q0 AC Q0 DT 01 DT 01

Q00843 Q00843; Q1-NOV-1996 Q1-NOV-1996 Q1-NOV-1998

(TrEMBLrel.

Created)

PRELIMINARY;

PRT;

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(TrEMBLrel.

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RE Science 287:2185-2195(2000).
REMBL, AE003448; AAP46516.1; -.
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Best Local Similarity
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InterPro; IPR003101; -.
Pfam; PF00439; bromodomain; 1
Pfam; PF00569; ZZ; 1.
Pfam; PF02135; zf-TAZ; 2.
Pfam; PF02172; KIX; 1.
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1622
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PROSITE; PS50014; BROMODOMAIN_2;
SMART; SM00297; BROMOD 1.
SEQUENCE 3275 AA; 340672 MW;
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InterPro; IPR000197; -.
InterPro; IPR000433; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 TPLDFSALSGKSPQPNTFGEQN--TQQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDAS 71
                                       QEVTIDNVHAQNVGEDLITVKGEGGAAV----TNLNIKNSSAKGADDKVVQLNANTHLK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGL---GTP---- 124
  EAMDYDEAGGSTAGEH - - - - HGEGGGGSGVGGGKDNINGAHDGGATGGAVDIKPKTETK
                                                                                   EFMDDSCGGNNDSSQ----MDCSTGGGKGKNVNNDGTSMIKMEIKTEDGLDG-EVKIK-T
                                                                                                                           TFTADKSMGNGDQGENQKPMFELAEGATLKNVN------LGENEVDGIHVKAKNA 293
                                                                                                                                                                     ARDNDDETPSPSGENTNGSGGSGN----AGGMASKGKLDSIKQDDDIK------K 1567
                                                                                                                                                                                           ---AGGGSSTTPASNPLLLMSGGTAGGGTGATTTTSTSSSSRMMSSSSSLSSQMAALEAA 1522
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                                                                                                                                                                                                                                                                                                                                                                                ----SADSGGGGTPDATGGGGGDTPSATGGGGG------DTPTA-----TGGGGSGGGGT 169
                                                                                                                                                                                                                                                                                                                                                                                                                          SANNNPPSVSSLMQ------QPLSN---RPGTPPYIPASPVPATSASGLAASSTPASAA 1405
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AA; 3
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25.1%;
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Pred. No. 7
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P93658;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica napus (Rape).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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EMBL; U13049; AAA87382.1; -.
                                                                                                                                                                                                                                                                                                          EMBL; Y11483; CAA72271.1;
HSSP; P18670; 1JAC.
                                                                                                                                                                                                                                                                                                                                                             Geshi N., Brandt A.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-GLOBAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Y--DRGSGACKGQNEGGDKDAVFLLHEGATLKNVIIGKDQSEGVHCKG----HCTLEFVW
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Pred. No. 6.7e-06;
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Pred. No. 4.3e-05;
3; Mismatches 139;
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyase.
SEQUENCE
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Guo W., Gonzalez-Candelas L., Kolattukudy P.E.;
"Identification of a novel pelD gene expressed uniquely in planta
Fusarium solani f. sp. pisi (Nectria haematococca, mating type VI)
characterization of its protein product as an endo-pectate lyase."
Arch. Biochem. Biophys. 332:305-312(1996).
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01-MAY-1999
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                                                                                                                                235 AGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQ 294
                                                                                                                                                                                                                                                                    175 GGSGGTPTATGGGEGGVTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443
                               295 EVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 QTYDGIGAVKFVYNKGSSEIIGDEHGKSTLLGFEEFELNYPSEYI--TEVHGTYDKISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 TGFHGRAGATISAIGVYLAPVGTIPLTPATQTKKLEAKGGDGGTTWDDGAFDGIRKVSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
99
                                                                                                                                                                                                                   21 GYTGGVPKATG-----SKSLSAPK-----
SCNIEFAWFEDVCEDAISILGSGTA ---- NIIGGGAYHASDKVIQHNGCGHVNIVNFYA 153
                                                                                                       KGEVFDAGWVRYDRGVKCSGQAEGGSKDAVFILEEGATLRNVIIGANQREGIHCKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEEFELASDEYITIVEGYYDKILGSDGLTSLTFHTNKGTYGPYGLEGSTHFEFKEDGHKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGESGAVWDDGAHDNVKKVSVGQ-----GTDGIAAVKFEYRNGSSVVIGAERGTPTLLG
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72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA;
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                                                                                                                                                                                                                                                                                                                             Conservative
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1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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RESULT 15
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AC Q21835
AC Q21835
DT 01-NOV
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Best Local :
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; Z68008; CAA92000.1; -.
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      876 GSGGGGSNSNSGGGGGGGGGGG-----AGAGNGNG
                                                              148 TGGGGGDTPTATGGGSGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSG
                                                                                                                                                                                                                                                 770 HNTRNL----AKLMTRAVQK--RFGTTFESVVAEADFSWGTNKFNGRTCKIDS-----
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                                                                                                                                                                                     QMLTNSNKKQDTNQEQPDSQ-APFQNNGGLGTPSADSGGGG----TPDATGGGGGDTPSA 147
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Search completed: October 4, 2001, 22:33:09 Job time: 395 sec

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MEDLINE
REFERENCE
AUTHORS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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JOURNAL
                                          Query Match
Best Local Similarity
Matches 694; Conser
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U16119.1
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Pseudomonas syringae p
transcriptional units
                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 710)
Keen, N.T.
                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 710)
Lorang, J.M. and Keen, N.T.
Characterization of avrE from Pseudomonas syringae
hrp-linked avirulence locus consisting of at least
transcriptional units
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas syringae
Pseudomonas syringae
                                                                                                                                                                                                                                                                                  Submitted (18-OCT-1994) Noel T. Keen, Plant Pathology, of California at Riverside, Riverside, CA 92521, USA
                                                                                                                                                                                                                                                                                                                                                                                                                          pseudomonas syringae pv. t
pseudomonas syringae pv. t
Bacteria; Proteobacteria;
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                                             Conservative
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                                                                                                      /evidence=not_experimental
/product="unknown"
/protein_id="aAC43432.1"
/db_xref="G1:563241"
/tanslation="MPLTSSKLNPKHPHPYRTDSDTATCSGKPWSWRRSNCPLSEVTQ
/translation="MPLTSSKLNPKHPHPYRTDSDTATCSGKPWSWRRSNCPLSEVTQ
HEIRHHTPAATDHHAARFFGAKROESSTKHVRRAEHSASDRPECTVVRQRHTERRQLR
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/db_xref="taxon:323"
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Erwinia amylovora
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HrpW of Erwinia amylovora, a new harpin that contains homologous to pectate lyases of a distinct class J. Bacteriol. 180 (19), 5203-5210 (1998)
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Direct Submission
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2 (bases 1 to 2708)
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Submitted (18-MAR-1997)
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